

QY	1	ATTAAACAGGCCCGTGGTTAGGAGAGACGAGAAAGGAGCGTTGCTCCTTTGGACCTTTTCA	60
Db	1	ATTAAACAGGCGCGTGGTTAGGAGAGACGAGAAAGGAGCGTTGCTCCTTTGGACCTTTTCA	60
QY	61	TGCGTCGTTTTTTTTTTCAGAGTGTGGCTGTGGCTGGGGCGCAAGGTCCGAGCAGCAGCTTA	120
Db	61	TGCGTCGTTTTTTTTTTCAGAGTGTGGCTGTGGCTGGGGCGCAAGGTCCGAGCAGCAGCTTA	120
QY	121	AGCTTACTCTTTCTGTGAAAGGGGAAAGTATCCCTGTGAAAAGCGTGTAAACCTTGTGAG	180
Db	121	AGCTTACTCTTTCTGTGAAAGGGGAAAGTATCCCTGTGAAAAGCGTGTAAACCTTGTGAG	180
QY	181	GGGGTGGGGGACGTGAATTTCTCCCAATGCACAGCGAAATGTGTGGCTTGAGCTGATCC	240
Db	181	GGGGTGGGGGACGTGAATTTCTCCCAATGCACAGCGAAATGTGTGGCTTGAGCTGATCC	240
QY	241	AGGAGCGGGCTCGACGTGTCTGAGAGGAGCCCGGAGGGGAGCGGGAGAGTGTGACCCACAGAA	300

Db	241	AGGAGCCGCGCTCGACGCTGTCTGAGGGAGGCGCGAGGGGGCGGGAGGCTGCGCCACAGAA	300
Qy	301	CGCGGGTCTGTAAAGAGAGCTTGGGAGAAATTCGATTCGAGAAAGGAGAAACCGGATT	360
Db	301	CGCGGGTCTGTAAAGAGAGCTTGGGAGAAATTCGATTCGAGAAAGGAGAAACCGGATT	360
Qy	361	GAAGAAGAGCGAGCGCTGAGGGGGAGGGGGCTGTGAAGATGCGCTCTCTCCGG	420
Db	361	GAAGAAGAGCGAGCGCTGAGGGGGAGGGGGCTGTGAAGATGCGCTCTCTCCGG	420
Qy	421	GGCGTGTCTTCGGTGGGTTTTCACTCTTGAATCCCGGGGCGCTTCCTGTACCTTGTGC	480
Db	421	GGCGTGTCTTCGGTGGGTTTTCACTCTTGAATCCCGGGGCGCTTCCTGTACCTTGTGC	480
Qy	481	CTCAGACCTGGAATCAAGAGACCCAGTGGCATCTGAGGTGCTTATGCTTCGCGATGCC	540
Db	481	CTCAGACCTGGAATCAAGAGACCCAGTGGCATCTGAGGTGCTTATGCTTCGCGATGCC	540
Qy	541	CATCAAGAAAATAGCGCATAGAAGTGTGAATTCCTCAGAGAGACAAATATTAAGAAC	600
Db	541	CATCAAGAAAATAGCGCATAGAAGTGTGAATTCCTCAGAGAGACAAATATTAAGAAC	600
Qy	601	AACCCATCAGCCCTTGAAAGGTGCGATCCAGTTAGGCAATTACCACTGAGGGGAGCT	660
Db	601	AACCCATCAGCCCTTGAAAGGTGCGATCCAGTTAGGCAATTACCACTGAGGGGAGCT	660
Qy	661	GAGTACCAAAACAGAGCGGTATGCTCTCATGCAAGATTTCTACGTGGTTGAGAGTATCTT	720
Db	661	GAGTACCAAAACAGAGCGGTATGCTCTCATGCAAGATTTCTACGTGGTTGAGAGTATCTT	720
Qy	721	CTTTTCCAGTGAAGGAGGCAACTGACCCCTGCTCATCATCATATGACTTTTCGTTCAA	780
Db	721	CTTTTCCAGTGAAGGAGGCAACTGACCCCTGCTCATCATCATATGACTTTTCGTTCAA	780
Qy	781	GACCGTATGCACTGTGTGCGCTTCCGCGTACTTCCGGAGCTAATTTGGATTCGGGCCGATGA	840
Db	781	GACCGTATGCACTGTGTGCGCTTCCGCGTACTTCCGGAGCTAATTTGGATTCGGGCCGATGA	840
Qy	841	TTACTTGTATTCCTCCTGCGAGTGAAGCGCGTGAATGGAATCTGTAGCTCTGAGGCTAGTG	900
Db	841	TTACTTGTATTCCTCCTGCGAGTGAAGCGCGTGAATGGAATCTGTAGCTCTGAGGCTAGTG	900
Qy	901	TTCCCTATTTCTATGTGTGTCACGCGATGATGTTCAATTAAGACAGTTCCAACATTAAGA	960
Db	901	TTCCCTATTTCTATGTGTGTCACGCGATGATGTTCAATTAAGACAGTTCCAACATTAAGA	960
Qy	961	GGCGGAAATTTCTGAGAAAGCGCTTCCAGGATCTCATGAACCTCAACCGAACCCCTCG	1020
Db	961	GGCGGAAATTTCTGAGAAAGCGCTTCCAGGATCTCATGAACCTCAACCGAACCCCTCG	1020
Qy	1021	GACTTGTGCTCAAAATTTCTATGAGCTGTACTGTGTGCAAGGAGGTCGAGAAACATTG	1080
Db	1021	GACTTGTGCTCAAAATTTCTATGAGCTGTACTGTGTGCAAGGAGGTCGAGAAACATTG	1080
Qy	1081	GATTGTGTGTATGAACAATCTTTTACCAAGATGTGTAAATATGATATGATGACT	1140
Db	1081	GATTGTGTGTATGAACAATCTTTTACCAAGATGTGTAAATATGATATGATGACT	1140
Qy	1141	CAAAAGGCTCAACCTACAAAGGGGGGCTTCCAGAAAGAGCGAGAGAAAGCTCTTCCAC	1200
Db	1141	CAAAAGGCTCAACCTACAAAGGGGGGCTTCCAGAAAGAGCGAGAGAAAGCTCTTCCAC	1200
Qy	1201	ATTTAAGAAGCTAGACTTCTTACAAAGACATCCCTGATGCTTTTATTTGGATGCTGACAT	1260
Db	1201	ATTTAAGAAGCTAGACTTCTTACAAAGACATCCCTGATGCTTTTATTTGGATGCTGACAT	1260
Qy	1261	GTACAAAGCTCTCTGTAAAGACCTTGACAGCTGACTGTTTGTGTGCTGACAGCTTCAGAT	1320
Db	1261	GTACAAAGCTCTCTGTAAAGACCTTGACAGCTGACTGTTTGTGTGCTGACAGCTTCAGAT	1320
Qy	1321	AATGATTAACAGCTCTTGATGTCAATCCATAATATTAAGATGACGCAACGAGAGCCCTT	1380
Db	1321	AATGATTAACAGCTCTTGATGTCAATCCATAATATTAAGATGACGCAACGAGAGCCCTT	1380

D	b	1321	AATGGATTACAGGCTCTTGATGATCAATCCATTAATATAGATATATGACACAAAGAGACCCCTT	1380
Q	y	1381	AAGCAGTGAAGCAACAGTACTCTCAAGTTGATATCTGAAGACCCGGCCCCCAAAAGGCTCTGTA	1440
D	b	1381	AAGCAGTGAAGCAACAGTACTCAAGTTGATATCTGAAGACCCGGCCCCCAAAAGGCTCTGTA	1440
Q	y	1441	TTCCACAGCCATGAATTCATCCAGGAGAGAGGCTGACCGGGGTGGTACATGAGACCTGA	1500
D	b	1441	TTCCACAGCCATGAATTCATCCAGGAGAGAGGCTGACCGGGGTGGTACATGAGACCTGA	1500
Q	y	1501	TGACCATATGGGTGGCATCCCTGCCGGAAATGTAAGGGGAAAGGCTCTGCTTTATAT	1560
D	b	1501	TGACCATATGGGTGGCATCCCTGCCGGAAATGTAAGGGGAAAGGCTCTGCTTTATAT	1560
Q	y	1561	TGGCATATTGAACATTTCTACAGTCTTACAGGTTTGTAAAGAGTTGGAGCATCTTGGAA	1620
D	b	1561	TGGCATATTGAACATTTCTACAGTCTTACAGGTTTGTAAAGAGTTGGAGCATCTTGGAA	1620
Q	y	1621	AGCCCTGTATCATGACGGAGACACTGTCTCAGTGCATGCCACAGCTTCTACGCTGACG	1680
D	b	1621	AGCCCTGTATCATGACGGAGACACTGTCTCAGTGCATGCCACAGCTTCTACGCTGACG	1680
Q	y	1681	GTTCACAGCGCTTCATGTGCACAACAAGTATTTAAGAAATTCCTTGAAGCCTTCTCCTTC	1740
D	b	1681	GTTCACAGCGCTTCATGTGCACAACAAGTATTTAAGAAATTCCTTGAAGCCTTCTCCTTC	1740
Q	y	1741	CAAAAATGTTCCGTCTGGGCTCATCTTTCTCTCGGGAGACAGGCTCCAGTGCACATCTCG	1800
D	b	1741	CAAAAATGTTCCGTCTGGGCTCATCTTTCTCTCGGGAGACAGGCTCCAGTGCACATCTCG	1800
Q	y	1801	CATTACTTACACAGCAATCCGCTCTCTGGGAGACAAACAAGCACAAGTGAACAACAAAGGACGA	1860
D	b	1801	CATTACTTACACAGCAATCCGCTCTCTGGGAGACAAACAAGCACAAGTGAACAACAAAGGACGA	1860
Q	y	1861	AGTGAAGCAGGCGTTTCAACCTTGTGTGTCCTGATGTTTTTACCTCAGACTCACCCTTTGGA	1920
D	b	1861	AGTGAAGCAGGCGTTTCAACCTTGTGTGTCCTGATGTTTTTACCTCAGACTCACCCTTTGGA	1920
Q	y	1921	GGAATTCAGTGAAGGCTCGCTCATTTCTCTGAACCCCAAGTTTCTCACCCTCAAGTTGGAGAGAC	1980
D	b	1921	GGAATTCAGTGAAGGCTCGCTCATTTCTCTGAACCCCAAGTTTCTCACCCTCAAGTTGGAGAGAC	1980
Q	y	1981	TTTGGAAATGCTAACCTACAAAGTCAACCTTGGAAAAGCTGAAAGTGCAGAGTACAGATT	2040
D	b	1981	TTTGGAAATGCTAACCTACAAAGTCAACCTTGGAAAAGCTGAAAGTGCAGAGTACAGATT	2040
Q	y	2041	CACCCATTAAACCGCAAGGCTTCAGAAAGACCTGGAACAAGATTCTGCATCTCTGTGATCC	2100
D	b	2041	CACCCATTAAACCGCAAGGCTTCAGAAAGACCTGGAACAAGATTCTGCATCTCTGTGATCC	2100
Q	y	2101	CAGATGTCAAGCTTGTCCCTCCACAGATGCTGAAATTTTCTTCTACCTTGGTCAATCAAAAAG	2160
D	b	2101	CAGATGTCAAGCTTGTCCCTCCACAGATGCTGAAATTTTCTTCTACCTTGGTCAATCAAAAAG	2160
Q	y	2161	GAGGTAAATTAAGATGAGGGAGACTGCTCCTCATCTTCTCTGAAGAAACACTTCTC	2220
D	b	2161	GAGGTAAATTAAGATGAGGGAGACTGCTCCTCATCTTCTCTGAAGAAACACTTCTC	2220
Q	y	2221	TGCTTCTCTTCTCATGAAATGAGGCTTAAGTGCTTCAGAGATTGAGGACCGCAGCATCC	2280
D	b	2221	TGCTTCTCTTCTCATGAAATGAGGCTTAAGTGCTTCAGAGATTGAGGACCGCAGCATCC	2280
Q	y	2281	CCTCCATCTCAAGATGGGTGGTGTACGGATTTTCAACTGGCCAAACCTTTGGCTCCACAT	2340
D	b	2281	CCTCCATCTCAAGATGGGTGGTGTACGGATTTTCAACTGGCCAAACCTTTGGCTCCACAT	2340
Q	y	2341	TGAATTTTTCACACCCCAATTTCTTACGTGGAATGGGATTCCTGACCTTGGCAGCT	2400
D	b	2341	TGAATTTTTCACACCCCAATTTCTTACGTGGAATGGGATTCCTGACCTTGGCAGCT	2400
Q	y	2401	TTCTTCCCTCTGTCTTGACTAGAGAACCGGACTCTTAATTTTCTCAAGACAGACTAGCT	2460
D	b	2401	TTCTTCCCTCTGTCTTGACTAGAGAACCGGACTCTTAATTTTCTCAAGACAGACTAGCT	2460

QY 2461 GGACATTATCCCTACCTTAGTCTTTCTCTGACTCCTGGAAATATCTCTGATC 2520
 DB 2461 GGACATTATCCCTACCTTAGTCTTTCTCTGACTCCTGGAAATATCTCTGATC 2520
 QY 2521 TCTGTAAAGTCTTTGGGGGATTAAGGGGTTTAACCACTCCGAGCTTCTTCTTTT 2580
 DB 2521 TCTGTAAAGTCTTTGGGGGATTAAGGGGTTTAACCACTCCGAGCTTCTTCTTTT 2580
 QY 2581 TTTTCTGAAAAAGAAAAAGCAACAGACACAAATTTGAAGCCATTTTCAGATCAGA 2640
 DB 2581 TTTTCTGAAAAAGAAAAAGCAACAGACACAAATTTGAAGCCATTTTCAGATCAGA 2640
 QY 2641 ACTCAGAGTGTGACAAAGATGCTTATCGTAGTTCCTCAGAAAGCCATGAGTGT 2700
 DB 2641 ACTCAGAGTGTGACAAAGATGCTTATCGTAGTTCCTCAGAAAGCCATGAGTGT 2700
 QY 2701 TATGAAAGAAAGATGATGATGCTCTGCGAAGAACAGCTCTCTTTAACTCTCTCT 2760
 DB 2701 TATGAAAGAAAGATGATGATGCTCTGCGAAGAACAGCTCTCTTTAACTCTCTCT 2760
 QY 2761 CTGTATGATTTCTTAAGGCTGAAGGATGAAGAGAGTGGACATGGGTATCTTTATC 2820
 DB 2761 CTGTATGATTTCTTAAGGCTGAAGGATGAAGAGAGTGGACATGGGTATCTTTATC 2820
 QY 2821 CCTTTTGTAAAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2880
 DB 2821 CCTTTTGTAAAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2880
 QY 2881 TCTGTCTACTCCAGGCTATGATTAATTAATTTTGAATTTGAATTAATTTCTG 2940
 DB 2881 TCTGTCTACTCCAGGCTATGATTAATTAATTTTGAATTTGAATTAATTTCTG 2940
 QY 2941 TTTTCTTTCTTAAGTGAAGCTTAACCAATGAATTTTGAATTTCTCCAGAGAGATT 3000
 DB 2941 TTTTCTTTCTTAAGTGAAGCTTAACCAATGAATTTTGAATTTCTCCAGAGAGATT 3000
 QY 3001 TTTTCTCTCTCTCACTCTTTTCCAAAGTGTCTCTGTTTGAAGCTTAAGGTTAAAGA 3060
 DB 3001 TTTTCTCTCTCTCACTCTTTTCCAAAGTGTCTCTGTTTGAAGCTTAAGGTTAAAGA 3060
 QY 3061 GGGGAGCACTTCTGTCTGTTTAAAGAGAGTCAATCTGTGAGGCGAGCAATATTTCT 3120
 DB 3061 GGGGAGCACTTCTGTCTGTTTAAAGAGAGTCAATCTGTGAGGCGAGCAATATTTCT 3120
 QY 3121 TAACTATGAGGAG 3180
 DB 3121 TAACTATGAGGAG 3180
 QY 3181 CTACCCCCCTGTCTTCAAGCAGAGAGTGAAGTGGGGGCTACATATGCCCTCTCC 3240
 DB 3181 CTACCCCCCTGTCTTCAAGCAGAGAGTGAAGTGGGGGCTACATATGCCCTCTCC 3240
 QY 3241 CCGTCTAACAAGAGTGTGTTTTCATCTGATCCTTCACTCTGTCAAGGGAAGAGG 3300
 DB 3241 CCGTCTAACAAGAGTGTGTTTTCATCTGATCCTTCACTCTGTCAAGGGAAGAGG 3300
 QY 3301 GGGCTGTATCTCAGGAGAGATGTTGAATCTGTCTATCCCTCTATCCACCTG 3360
 DB 3301 GGGCTGTATCTCAGGAGAGATGTTGAATCTGTCTATCCCTCTATCCACCTG 3360
 QY 3361 CCTGTAATATGTTAGGCCATACCCCAATATGCTATATTAAGACACCCGAGCAG 3420
 DB 3361 CCTGTAATATGTTAGGCCATACCCCAATATGCTATATTAAGACACCCGAGCAG 3420
 QY 3421 TTTCTGCTGCTGTCTTGTGCTGATGTTTAAACAAGAGAAAGATTTCTGATTT 3480
 DB 3421 TTTCTGCTGCTGTCTTGTGCTGATGTTTAAACAAGAGAAAGATTTCTGATTT 3480
 QY 3481 TTTTCTCATATTAATTAATTAAGTATTAAGTGTTTTAAAGAGAGAGAGTCTG 3540
 DB 3481 TTTTCTCATATTAATTAATTAAGTATTAAGTGTTTTAAAGAGAGAGAGTCTG 3540

QY 3541 TTAGGGGTGGAGGAAATTTGAGGAGGCTGGCTTTAGGGAAGAAATGGGAGC 3600
 DB 3541 TTAGGGGTGGAGGAAATTTGAGGAGGCTGGCTTTAGGGAAGAAATGGGAGC 3600
 QY 3601 AACATTTTATTAAGTGTACTATTTGCTGTACTTTGTATTTGTCAGAAATGGCAATA 3660
 DB 3601 AACATTTTATTAAGTGTACTATTTGCTGTACTTTGTATTTGTCAGAAATGGCAATA 3660
 QY 3661 CAATATTAAGTATATGTTTAAATGTAATTAATTAATTAATTAATTAATTAATTA 3713
 DB 3661 CAATATTAAGTATATGTTTAAATGTAATTAATTAATTAATTAATTAATTAATTA 3713

RESULT 2 US-09-949-016-513

; Sequence 513, Application US/09949016
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: C1001307
 ; CURRENT APPLICATION NUMBER: US/09/949, 016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 513
 ; LENGTH: 3713
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-513

Query Match 100.0%; Score 3713; DB 7; Length 3713;
 Best Local Similarity 100.0%; Pred No. 0;
 Matches 3713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTAACAGGCGGTGTAG 60
 DB 1 ATTAACAGGCGGTGTAG 60
 QY 61 TGCTCGTTTTTTTCAAGATGAGCTTGTGAGGCGAAGGTCCTTGGAGCTTTTCA 120
 DB 61 TGCTCGTTTTTTTCAAGATGAGCTTGTGAGGCGAAGGTCCTTGGAGCTTTTCA 120
 QY 121 AGCTTACTCTCTGTGAAGAGGGAAGATCCCTGTGGAAGCGGTTAACTTTGAG 180
 DB 121 AGCTTACTCTCTGTGAAGAGGGAAGATCCCTGTGGAAGCGGTTAACTTTGAG 180
 QY 181 GGGGTGAGGAGAGGAGTCTTCCCATGCGAGAGATGATGAGGCTTGAAGCTGCTC 240
 DB 181 GGGGTGAGGAGAGGAGTCTTCCCATGCGAGAGATGATGAGGCTTGAAGCTGCTC 240
 QY 241 AGAGAGCGGCTCGAGCTGTGAGAGAGGCGGAGGAGGAGGAGGAGGAGGAGGAG 300
 DB 241 AGAGAGCGGCTCGAGCTGTGAGAGAGGCGGAGGAGGAGGAGGAGGAGGAGGAG 300
 QY 301 CGGGGTTCTGTAAAGAGAGTGGGAAGATTCGATTCGAGAAAGAGAGAACCGGATT 360
 DB 301 CGGGGTTCTGTAAAGAGAGTGGGAAGATTCGATTCGAGAAAGAGAGAACCGGATT 360
 QY 361 GAAAGAGAGCAGGCGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
 DB 361 GAAAGAGAGCAGGCGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
 QY 421 GCGGTGCTTCTGCTGCTGCTTCTTCAATCCTTGAATCCGCGGTCCTTCTGATCTTGT 480
 DB 421 GCGGTGCTTCTGCTGCTGCTTCTTCAATCCTTGAATCCGCGGTCCTTCTGATCTTGT 480

QY 481 CTGAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCTTATGCTCTGCGATGCC 540
 DB 481 CTGAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCTTATGCTCTGCGATGCC 540
 QY 541 CATCAAGAAATAGGCCATAGAGGTGATTCCTCAGAGAGACAACATATAAAGAGAC 600
 DB 541 CATCAAGAAATAGGCCATAGAGGTGATTCCTCAGAGAGACAACATATAAAGAGAC 600
 QY 601 AACCTCATCAGCCTTGAAGAGGTGCATCAGTTAGGCATTAACCACTGTGGAGAGCT 660
 DB 601 AACCTCATCAGCCTTGAAGAGGTGCATCAGTTAGGCATTAACCACTGTGGAGAGCT 660
 QY 661 GAGTACCAACCAAGAGGTGATTCCTCATGCAAGATTTCTACGTGTGGAGATTCCT 720
 DB 661 GAGTACCAACCAAGAGGTGATTCCTCATGCAAGATTTCTACGTGTGGAGATTCCT 720
 QY 721 CTTTCCAGTGAAGGAGAGCAACCTGACCCCTGCTCATCACTACATGACTTTCGTTCAA 780
 DB 721 CTTTCCAGTGAAGGAGAGCAACCTGACCCCTGCTCATCACTACATGACTTTCGTTCAA 780
 QY 781 GACCTATGCACTGTGTGCTTCGCTACTTCGAGAGCTATTTGGATCCGGCCGATGA 840
 DB 781 GACCTATGCACTGTGTGCTTCGCTACTTCGAGAGCTATTTGGATCCGGCCGATGA 840
 QY 841 TTACTTGTATTCCTCTGAGTGAAGCCGCTGATTTGAATCTGTAGCTGTGAGCTAGTG 900
 DB 841 TTACTTGTATTCCTCTGAGTGAAGCCGCTGATTTGAATCTGTAGCTGTGAGCTAGTG 900
 QY 901 TTCCCTATTCATGTGTGTCAGAGAGATGATTCATTTAAGACAGTCCAACTAAGAGA 960
 DB 901 TTCCCTATTCATGTGTGTCAGAGAGATGATTCATTTAAGACAGTCCAACTAAGAGA 960
 QY 961 GCGGGAATTTCTGAGAGAGTCTTCAGAGATCTACATGAACTTCAACCAAGACCTTCG 1020
 DB 961 GCGGGAATTTCTGAGAGAGTCTTCAGAGATCTACATGAACTTCAACCAAGACCTTCG 1020
 QY 1021 GACTTTCGCTGAATTAATTTATGAGACTGATGTGTGAGAGAGGAGAGAACTTCG 1080
 DB 1021 GACTTTCGCTGAATTAATTTATGAGACTGATGTGTGAGAGAGGAGAGAACTTCG 1080
 QY 1081 GATTTGTGTATGAACTATTTTCAAGATCGGTAAATATGATATATGATGACT 1140
 DB 1081 GATTTGTGTATGAACTATTTTCAAGATCGGTAAATATGATATATGATGACT 1140
 QY 1141 CAAGAGCTCACTCAACACGCGGGCTTCAGAGAAAGGAGAGAGAGAGAGAGAGAG 1200
 DB 1141 CAAGAGCTCACTCAACACGCGGGCTTCAGAGAAAGGAGAGAGAGAGAGAGAGAG 1200
 QY 1201 AATTAAAGACTGATCTTCTTACAGACATCCCTGATGCTTTTGTGATGCTGATCAT 1260
 DB 1201 AATTAAAGACTGATCTTCTTACAGACATCCCTGATGCTTTTGTGATGCTGATCAT 1260
 QY 1261 GTACAAAGCTCTCTGTAGACCTTCGAGAGGTGATCTGTTGTGTGCTGAGAGCTTCA 1320
 DB 1261 GTACAAAGCTCTCTGTAGACCTTCGAGAGGTGATCTGTTGTGTGCTGAGAGCTTCA 1320
 QY 1321 AATGATTAAGAGCTCTTGTATGTCAATCCATATATATGATCATGCAACAGAGAGCTT 1380
 DB 1321 AATGATTAAGAGCTCTTGTATGTCAATCCATATATATGATCATGCAACAGAGAGCTT 1380
 QY 1381 AAGCAGTGAACACAGATCTCAGTTGATCTGAGAGAGAGAGAGAGAGAGAGAGAGCT 1440
 DB 1381 AAGCAGTGAACACAGATCTCAGTTGATCTGAGAGAGAGAGAGAGAGAGAGAGAGCT 1440
 QY 1441 TTCCAGAGCATGGAATCATCAAGAGAGAGAGCTCGAGGGGTGTGATCCATGAGACTGA 1500
 DB 1441 TTCCAGAGCATGGAATCATCAAGAGAGAGAGCTCGAGGGGTGTGATCCATGAGACTGA 1500
 QY 1501 TGACCAATATGGGTGATTCCTGCGGGAATGATTAAGAGAGAGAGAGAGAGAGAGAG 1560
 DB 1501 TGACCAATATGGGTGATTCCTGCGGGAATGATTAAGAGAGAGAGAGAGAGAGAGAG 1560
 QY 1561 TGGCATCATGACATTTCTACAGTCTTACAGGTTTGTAAAGATTTGAGAGACTTGGAA 1620

DB 1561 TGGCATCATGACATTTCTACAGTCTTACAGGTTTGTAAAGATTTGAGAGACTTGGAA 1620
 QY 1621 AGCCCTGTATCATGAGAGAGACTGTCTCATGATCATGCCCCAGGCTTTAGCTGAAG 1680
 DB 1621 AGCCCTGTATCATGAGAGAGACTGTCTCATGATCATGCCCCAGGCTTTAGCTGAAG 1680
 QY 1681 GTTCCAGAGCTTATGAGAGAGAGATTTAAGAGATTCCTCTGAGAGAGAGAGAGAGCT 1740
 DB 1681 GTTCCAGAGCTTATGAGAGAGAGATTTAAGAGATTCCTCTGAGAGAGAGAGAGAGCT 1740
 QY 1741 CAAAAAGTTTCGATGCTCATCTTCTCTGCGAGAGAGAGCTCCAGTGGCACTCTCG 1800
 DB 1741 CAAAAAGTTTCGATGCTCATCTTCTCTGCGAGAGAGAGCTCCAGTGGCACTCTCG 1800
 QY 1801 CATTACTTACAGAGCATCGGTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
 DB 1801 CATTACTTACAGAGCATCGGTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
 QY 1861 AGTGAAGCAGAGGCTTCACTTGTGCTGATGTTTAACTCAGACTCCACTTTGGA 1920
 DB 1861 AGTGAAGCAGAGGCTTCACTTGTGCTGATGTTTAACTCAGACTCCACTTTGGA 1920
 QY 1921 GGAATCATGAGAGGCTCGCTATTCCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
 DB 1921 GGAATCATGAGAGGCTCGCTATTCCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
 QY 1981 TTTCGAAATGCTATCATGATCAACCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040
 DB 1981 TTTCGAAATGCTATCATGATCAACCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040
 QY 2041 CACCATTAAAG 2100
 DB 2041 CACCATTAAAG 2100
 QY 2101 CAGATGCTAGAGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
 DB 2101 CAGATGCTAGAGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
 QY 2161 GAGTGAATGAAG 2220
 DB 2161 GAGTGAATGAAG 2220
 QY 2221 TCCCTTCCTCTCTCATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
 DB 2221 TCCCTTCCTCTCTCATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
 QY 2281 CCTCAGCTCAG 2340
 DB 2281 CCTCAGCTCAG 2340
 QY 2341 TGAATTTTTCAG 2400
 DB 2341 TGAATTTTTCAG 2400
 QY 2401 TTCTTTCCTCTCTCTCATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2460
 DB 2401 TTCTTTCCTCTCTCTCATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2460
 QY 2461 GGCACATTAATCCCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520
 DB 2461 GGCACATTAATCCCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520
 QY 2521 TCTGTAAGAGTTTGGGAGATTAAGAGATTAAGAGATTAAGAGATTAAGAGATTAAG 2580
 DB 2521 TCTGTAAGAGTTTGGGAGATTAAGAGATTAAGAGATTAAGAGATTAAGAGATTAAG 2580
 QY 2581 TTTTTCGAAAAAG 2640
 DB 2581 TTTTTCGAAAAAG 2640
 QY 2641 ACTCAG 2700

Db 2641 ACTCAGAGTGTGACAGAGATGCTTATTCGTAGAGTTCCTCAGAGAGCCATGATGTT 2700
 Qy 2701 TATGAGAGAGAGATGATGATGCTCTGCGCAGAGAGAGCTCCTCTTAACTCTCTCT 2760
 Db 2701 TATGAGAGAGAGATGATGATGCTCTGCGCAGAGAGAGCTCCTCTTAACTCTCTCT 2760
 Qy 2761 CTGATGATATTTCTTAAGGCTGAGAGATGAGAGAGAGAGATGAGAGATGAGAGATG 2820
 Db 2761 CTGATGATATTTCTTAAGGCTGAGAGATGAGAGAGAGAGATGAGAGATGAGAGATG 2820
 Qy 2821 CCTTTTGTAAACAG 2880
 Db 2821 CCTTTTGTAAACAG 2880
 Qy 2881 TCCGTGACGCGCAG 2940
 Db 2881 TCCGTGACGCGCAG 2940
 Qy 2941 TTTGTTTTCTAAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3000
 Db 2941 TTTGTTTTCTAAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3000
 Qy 3001 TTTTGTGCT 3060
 Db 3001 TTTTGTGCT 3060
 Qy 3061 GGGGACATTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 3120
 Db 3061 GGGGACATTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 3120
 Qy 3121 TAAATCTAGGAG 3180
 Db 3121 TAAATCTAGGAG 3180
 Qy 3181 CTACCCCCCTGCT 3240
 Db 3181 CTACCCCCCTGCT 3240
 Qy 3241 CCGCTCAAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 3300
 Db 3241 CCGCTCAAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 3300
 Qy 3301 GGGCTGATCTCAGGAG 3360
 Db 3301 GGGCTGATCTCAGGAG 3360
 Qy 3361 CCTGATATATGATGAG 3420
 Db 3361 CCTGATATATGATGAG 3420
 Qy 3421 TTTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480
 Db 3421 TTTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480
 Qy 3481 TTTTCTCATATTTCTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 3540
 Db 3481 TTTTCTCATATTTCTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 3540
 Qy 3541 TTTAGGAGTGGAGAGAGATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3600
 Db 3541 TTTAGGAGTGGAGAGAGATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3600
 Qy 3601 AAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 3660
 Db 3601 AAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 3660
 Qy 3661 CAATATTAAGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3720
 Db 3661 CAATATTAAGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3720

RESULT 3
 US-10-170-235-11868

; Sequence 11868, Application US/10170235
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig
 ; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
 ; FILE REFERENCE: C1001380
 ; CURRENT APPLICATION NUMBER: US/10/170,235
 ; CURRENT FILING DATE: 2003-03-17
 ; NUMBER OF SEQ ID NOS: 42514
 ; SEQ ID NO 11868
 ; LENGTH: 3707
 ; TYPE: DNA
 ; ORGANISM: HUMAN
 ; US-10-170-235-11868
 Query Match 96.3%; Score 3577; DB 8; Length 3707;
 Best Local Similarity 98.6%; Pred. No. 0;
 Matches 3663; Conservative 0; Mismatches 15; Indels 37; Gaps 4;
 Qy 1 ATTAACAGGCGGTGTTAG 60
 Db 28 ATTAACAGGCGGTGTTAG 87
 Qy 61 TGCCCTGTTTTTTTTTTCAGATGAGGCTTGTCTGAGGCGCAAGTCCAGAGAGAGAGTTA 120
 Db 88 TGCCCTGTTTTTTTTTTCAGATGAGGCTTGTCTGAGGCGCAAGTCCAGAGAGAGAGTTA 147
 Qy 121 AGCTTACTCTTCTGTGAAG 180
 Db 148 AGCTTACTCTTCTGTGAAG 207
 Qy 181 GGGGTGCGGAG 240
 Db 208 GGGGTGCGGAG 267
 Qy 241 AGAGCCGCGTGAAGTGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 299
 Db 268 AGAGCCGCGTGAAGTGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 327
 Qy 300 AGCGGGTCTGTGAAGAT 359
 Db 328 AGCGGGTCTGTGAAGAT 387
 Qy 360 TGAAG 419
 Db 388 TGAAG 447
 Qy 420 GGGCGTGTCTTGGAGTGTCTTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 479
 Db 448 GGGCGTGTCTTGGAGTGTCTTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 507
 Qy 480 CCTGAGATCTGGAATCAAG 539
 Db 508 CCTGAGATCTGGAATCAAG 535
 Qy 540 CCATCAAG 599
 Db 536 CCATCAAG 595
 Qy 600 CAACCTCATGAGCTTGAAG 659
 Db 596 CAACCTCATGAGCTTGAAG 655
 Qy 660 TGAATCAAG 719
 Db 656 TGAATCAAG 715
 Qy 720 TCTTTCCAG 779
 Db 716 TCTTTCCAG 775
 Qy 780 AGACCTATGACAGTGTGCTTCCGCTACTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 839

Db 776 AGACCTATGACCTGTGCTCCGCTACCTCCGGAAGCTATTGTTGATCCGGCCCGATG 835
Qy 840 ATTAATGATATTCCTCTGAGATGAGCCGCTGATGAACTCTGTAGCTCTGAGACTAGT 899
Db 836 ATTAATGATATTCCTCTGAGATGAGCCGCTGATGAACTCTGTAGCTCTGAGACTAGT 895
Qy 900 GTTCCCTATTTCTATGTGTCCAGGACGATGAGTTCATTTAAGACAGTCCAACTAAG 959
Db 896 GTTCCCTATTTCTATGTGTCCAGGACGATGAGTTCATTTAAGACAGTCCAACTAAG 955
Qy 960 AGGCGAATTTCTGAGAGAGCTCTCCAGAGTACTATGATCACTCAACGAGAACCTCTC 1019
Db 956 AGGCGAATTTCTGAGAGAGCTCTCCAGAGTACTATGATCACTCAACGAGAACCTCTC 1012
Qy 1020 GGAATTTCTGCTTAATTTCTATGAGCTGTACTGTGTGAGGAGGAGTGGCAAGAACTTC 1079
Db 1013 CACTTTTCTGCTTAATTTCTATGAGCTGTACTGTGTGAGGAGGAGTGGCAAGAACTTC 1072
Qy 1080 GGAATTTCTGCTTAATTTCTATGAGCTGTACTGTGTGAGGAGGAGTGGCAAGAACTTC 1139
Db 1073 GGAATTTCTGCTTAATTTCTATGAGCTGTACTGTGTGAGGAGGAGTGGCAAGAACTTC 1132
Qy 1140 TCAAGGCTCAACTACAAACGCGGCTTCCAGAAAGAGGAGAGGAGCTCTTCCCA 1199
Db 1133 TCAAGGCTCAACTACAAACGCGGCTTCCAGAAAGAGGAGAGGAGCTCTTCCCA 1192
Qy 1200 CATTAAAGACCTAGACTTTCTTACAAAGACATCCCTGATGTCTTTTGTGATGCTGAC 1259
Db 1193 CATTAAAGACCTAGACTTTCTTACAAAGACATCCCTGATGTCTTTTGTGATGCTGAC 1252
Qy 1260 TGTACAAAGCTCTCTGTAGAGCCCTGAGGAGGAGGAGTGTGTGAGGAGGAGCTTCAAGA 1319
Db 1253 TGTACAAAGCTCTCTGTAGAGCCCTGAGGAGGAGGAGTGTGTGAGGAGGAGCTTCAAGA 1312
Qy 1320 TAAATGATTAAGAGCTCTTGTATGTCAATCATATATATGATCATGACAAACGAGCCCT 1379
Db 1313 TAAATGATTAAGAGCTCTTGTATGTCAATCATATATATGATCATGACAAACGAGCCCT 1372
Qy 1380 TAAAGATGAAACACAGTACTGATGATGATCTGAAAGACCGGCCCCCAAAAGGCTCTGT 1439
Db 1373 TAAAGATGAAACACAGTACTGATGATGATCTGAAAGACCGGCCCCCAAAAGGCTCTGT 1432
Qy 1440 ATTCCAGACGATGAGATCATCATGAGGAGGAGGCTGACGAGGAGTGGTACATGAGACTG 1499
Db 1433 ATTCCAGACGATGAGATCATCATGAGGAGGAGGCTGACGAGGAGTGGTACATGAGACTG 1492
Qy 1500 ATGACCATATGAGGTGAGCATCCCTGCGGGAATGTAAGGAGGAGGCTTGTGCTTATTA 1559
Db 1493 ATGACCATATGAGGTGAGCATCCCTGCGGGAATGTAAGGAGGAGGCTTGTGCTTATTA 1552
Qy 1560 TTGGCATCTATGACATTTCTACAGTCTTACAGGTTTGTAAAGATGAGGAGCTCTTGA 1619
Db 1553 TTGGCATCTATGACATTTCTACAGTCTTACAGGTTTGTAAAGATGAGGAGCTCTTGA 1612
Qy 1620 AAGCCTGTGATACGAGGAGCACTGTCTCACTGATGAGCTCCAGGCTTCTACGCTGAAC 1679
Db 1613 AAGCCTGTGATACGAGGAGCACTGTCTCACTGATGAGCTCCAGGCTTCTACGCTGAAC 1672
Qy 1680 GGTTCAGGCTTCAATGTGACACAGTATTTAAGAAATTTCCCTTGAAGCTTCTCTT 1739
Db 1673 GGTTCAGGCTTCAATGTGACACAGTATTTAAGAAATTTCCCTTGAAGCTTCTCTT 1732
Qy 1740 CCAAAAAGTTTGGGTCTGCTGATCTTTCTCTGCGGAGAGAGGCTCCAGTGGAACTTCT 1799
Db 1733 CCAAAAAGTTTGGGTCTGCTGATCTTTCTCTGCGGAGAGAGGCTCCAGTGGAACTTCT 1792
Qy 1800 GCAATTAATCAAGCCTGCTCTGAGGAGAAACAAGGACAAAGTGAACAACAAGGACAG 1859
Db 1793 GCAATTAATCAAGCCTGCTCTGAGGAGAAACAAGGACAAAGTGAACAACAAGGACAG 1852
Qy 1860 AAGTGAAGCAGGAGGTTCACTTGTGTGTCTGATGATTTTAACTCAAGCTCAACTTTGG 1919
Db 1853 AAGTGAAGCAGGAGGTTCACTTGTGTGTCTGATGATTTTAACTCAAGCTCAACTTTGG 1912

Qy 1920 AGGAATCAATGAGGAGGCTGCGCTATCTGACCCAGTTTCTCACTAGTTGAGAGA 1979
Db 1913 AGGAATCAATGAGGAGGCTGCGCTATCTGACCCAGTTTCTCACTAGTTGAGAGA 1972
Qy 1980 CTTTGCAATGCTAATCAATGATCAACTTGTGAAAGCTTGAAGTTGACAGTCAAGT 2039
Db 1973 CTTTGCAATGCTAATCAATGATCAACTTGTGAAAGCTTGAAGTTGACAGTCAAGT 2032
Qy 2040 TCAACCATTAAGGCAAGGCTCAAGAGCTGTGAACAGATTCGACATCTGTGATC 2099
Db 2033 TCAACCATTAAGGCAAGGCTCAAGAGCTGTGAACAGATTCGACATCTGTGATC 2092
Qy 2100 CCAAGATGAGGCTGCGCCAGCAATGTGATTTTCTTACTTGTGATCAATAAAA 2159
Db 2093 CCAAGATGAGGCTGCGCCAGCAATGTGATTTTCTTACTTGTGATCAATAAAA 2152
Qy 2160 GGAATGTAATGAAAGTGAAGGAGCTGTCTCTCATCTTCTTCTGAAGAACTTCT 2219
Db 2153 GGAATGTAATGAAAGTGAAGGAGCTGTCTCTCATCTTCTTCTGAAGAACTTCT 2212
Qy 2220 CTCTTCTCTCTCTCTCATGATGAGGCTTGTAGTCTTCAAGAGTGAAGCCGAGATC 2279
Db 2213 CTCTTCTCTCTCTCTCATGATGAGGCTTGTAGTCTTCAAGAGTGAAGCCGAGATC 2272
Qy 2280 CCGTCACTCAGAGTGGGAGGAGTGAAGGATTTTCACTGAGCAACCTTGTCTCCACTA 2339
Db 2273 CCGTCACTCAGAGTGGGAGGAGTGAAGGATTTTCACTGAGCAACCTTGTCTCCACTA 2332
Qy 2340 TTGAATTTTCTGAGACCCCATTTCTTATGCTGGAATGGAATGCTGGAATTTGGCAGC 2399
Db 2333 TTGAATTTTCTGAGACCCCATTTCTTATGCTGGAATGGAATGCTGGAATTTGGCAGC 2392
Qy 2400 TTTCTTCTCTCTCTCTTGAATGAGAAACCGAGCTCTTAATTTCTGAGAGAGACTAGC 2459
Db 2393 TTTCTTCTCTCTCTCTTGAATGAGAAACCGAGCTCTTAATTTCTGAGAGAGACTAGC 2452
Qy 2460 TGGACATTTATCCCTACCTTATGTTCTTCTCTGATCTCTGAGAAATATCTCTGAT 2519
Db 2453 TGGACATTTATCCCTACCTTATGTTCTTCTCTGATCTCTGAGAAATATCTCTGAT 2512
Qy 2520 CTCTGTAAGGTTTGGGAGTAAGGAGTTTAACAACCTCCAGCTTCTTCTTCTTCTTCT 2578
Db 2513 CTCTGTAAGGTTTGGGAGTAAGGAGTTTAACAACCTCCAGCTTCTTCTTCTTCTTCTT 2572
Qy 2579 TTTTCTTCTGAAAAAGGAAAAAGCAACAGCAACAATTTCAAGCAATTTTCAATCA 2638
Db 2573 TTTTCTTCTGAAAAAGGAAAAAGCAACAGCAACAATTTCAAGCAATTTTCAATCA 2632
Qy 2639 GAACTCCAGAGTGTGAACAAGTGCCTATTCTGTAAGTTCCCTCAGAAAGCAATGAGT 2698
Db 2633 GAACTCCAGAGTGTGAACAAGTGCCTATTCTGTAAGTTCCCTCAGAAAGCAATGAGT 2692
Qy 2699 TTTATGAAGAGATGATGATGCTCTGCGCAAGAGAGCTCTTAACTCTCTTCT 2758
Db 2693 TTTATGAAGAGATGATGATGCTCTGCGCAAGAGAGCTCTTAACTCTCTTCTCT 2752
Qy 2759 CTCTGATGAATTTCTTAAAGCTGAAGATGAAGAGTGGACATGAGGATTAATCTT 2818
Db 2753 CTCTGATGAATTTCTTAAAGCTGAAGATGAAGAGTGGACATGAGGATTAATCTT 2812
Qy 2819 TCCCTTTGTTAAACAGAGGAGCCATGAGGCTGAGGATCATAGCCCTTCTAGGAG 2878
Db 2813 TCCCTTTGTTAAACAGAGGAGCCATGAGGCTGAGGATCATAGCCCTTCTAGGAG 2872
Qy 2879 AATCTGTTCACTGCGAGCTATGATATTTATTTACTATTTTGCATTTGAATAATCT 2938
Db 2873 AATCTGTTCACTGCGAGCTATGATATTTATTTATTTTGCATTTGAATAATCT 2932
Qy 2939 GGTGTTTCTTAATGTAAGACTTACCAATGAATTTTGAATCATTTCCAGAGGAGA 2998
Db 2933 GGTGTTTCTTAATGTAAGACTTACCAATGAATTTTGAATCATTTCCAGAGGAGA 2992

Query Match	96.3%	Score 3375.8	DB 11	Length 3707
Best Local Similarity	98.5%	Pred. No. 0		
Matches 3660	Conservative 3	Mismatches 15	Indels 37	Gaps 4

1 ATTAACAGGCGCTGGTTCGGAAGACGAGAGAGGCGCTTCCTCTTTGGACATTTTCA 60

Db	28	ATTAAACAGCCCGTGGTTAGGAAGGACGAGAAAGGAGCGTTCCGCTCTTTGGGACTTTTCA	87
Qy	61	TGCGCTGGTTTTTTTTTCAGATGTGGCTGGTCTGGCGCAGAGTCCACAGCCAGCTTA	120
Db	88	TGCGCTGGTTTTTTTTTCAGATGTGGCTGGTCTGGCGCAGAGTCCACAGCCAGCTTA	147
Qy	121	AGCTTACTCTTCTGTGAAGGGGAAAGTATCCCTGTGGAAAGCGGTTAACTTGTGAG	180
Db	148	AGCTTACTCTTCTGTGAAGGGGAAAGTATCCCTGTGGAAAGCGGTTAACTTGTGAG	207
Qy	181	GGGGGCGGAGCGTGAAGTCTTCCCGCATGCGAGGCGAAATGATGTGGCCCTTGAGCTGGTCC	240
Db	208	GGGGTCCGGGACGTGAATTTCTTCCCATGCGAGGCGAAATGATGTGGCCCTTGAGCTGGTCC	267
Qy	241	AGAGCCGGCTCGACGTGTCTGAGGAGG-CCCGAGGGGGGCGGGAGGTGGCCCAAGA	299
Db	268	AGGAGCCGGCTCGACGTGTCTGAGGAGGCCCGAGGGGGGCGGGAGGTGGCCCAAGA	327
Qy	300	ACGCGGGTCTGTAAAGAGACGTTGGGAAAGTTCCATTCCGAAAGAGAGAACCGGAT	359
Db	328	ACGCGGGTCTGTAAAGAGACGTTGGGAAAGTTCCATTCCGAAAGAGAGAACCGGAT	387
Qy	360	TGAAGAAGACGACGCCGCTGAGGGGAGGGGGCTTAAGTGGCGTCCGCTCTCCG	419
Db	388	TGAAGAAGACGACGCCGCTGAGGGGAGGGGGCTTAAGTGGCGTCCGCTCTCCG	447
Qy	420	GGCGGTGTCTGGTGGTGGTTTTTCATCCCTTGGATCCCGGGTCCCTTCTGTACTTGT	479
Db	448	GGCGGTGTCTGGTGGTGGTTTTTCATCCCTTGGATCCCGGGTCCCTTCTGTACTTGT	507
Qy	480	CCTGAGCATCTGAAATCMAAGACCCATGGCATCTGAGGGTGCCTTATGGCTTGAGCATGC	539
Db	508	CCTC-----AGTGCCTTATGTCTCTGGCATGC	535
Qy	540	CCATCAGAAATATGGGCATATGAAGTGTGATTCCCTCAGAGAAAGCAACTTTAAAGA	599
Db	536	CCATCAGAAATATGGGCATATGAAGTGTGATTCCCTCAGAGAAAGCAACTTTAAAGA	595
Qy	600	CAACCTCATCAGCCTTGAAGGTCATCAAGTGAAGGCAATTAACCACTGCGGGAGCC	659
Db	596	CAACCTCATCAGCCTTGAAGGTCATCAAGTGAAGGCAATTAACCACTGCGGGAGCC	655
Qy	660	TGAGTACCAACCAAGACGCGTATGTCTCATGCAAGATTTCTAGCGTGTGAGATCT	719
Db	656	TGAGTACCAACCAAGACGCGTATGTCTCATGCAAGATTTCTAGCGTGTGAGATCT	715
Qy	720	TCTTTCCCACTGAAGGGAAGCACTTGAACCCCTGTCTCATCTACATGACTTGGTTCA	779
Db	716	TCTTTCCCACTGAAGGGAAGCACTTGAACCCCTGTCTCATCTACATGACTTGGTTCA	775
Qy	780	AGACCTATGACGCTGGTCCCTCCGCTACTCCGGAGCTATTTGATCCGGCCCGATG	839
Db	776	AGACCTATGACGCTGGTCCCTCCGCTACTCCGGAGCTATTTGATCCGGCCCGATG	835
Qy	840	ATTACTGTATTTCCCTCTGCACTGAGCAGCTGATTTGAATCTGTAGCTCTGGAGCTAGTG	899
Db	836	ATTACTGTATTTCCCTCTGCACTGAGCAGCTGATTTGAATCTGTAGCTCTGGAGCTAGTG	895
Qy	900	GTTCCTTATTTCTATGTGTCCAGCGAGTGAAGTTCAATTTAAGACAGTCCCAACTAAG	959
Db	896	GTTCCTTATTTCTATGTGTCCAGCGAGTGAAGTTCAATTTAAGACAGTCCCAACTAAG	955
Qy	960	AGGGGGAATTTCTGCAAGAGCTGCTCCAGGATPACTACATGAACTCAACCAAGACCTC	1019
Db	956	AGGGGGAATTTCTGCAAGAGCTGCTCCAGGATPACTACATG--GTAAAGGAGAGAGAAG	1012
Qy	1020	GAACCTTGTCTGCTAAATTTCTATGACTGTACTGTGTGCGAGCAGATGGCAAGACATTC	1079
Db	1013	CACCTTTGTCTGCTAAATTTCTATGACTGTACTGTGTGCGAGCAGATGGCAAGACATTC	1072
Qy	1080	GGATTGTGTGATGAACATCTTTTACCAAGTCCGTAAAAATGCAATCAATATGACC	1139

Db	1073	GGATTGTGTGATGACAACTCTTTTACCAAGATCGTAAAAATGATACATACAAATATGACC	1132
Qy	1140	TCAAAGGCTCAA CTTACAAACGGCGGGCTTCCAGAAAAGCGAGAGAAAGCTCTTCCCA	1139
Db	1133	TCAAAGGCTCAA CTTACAAACGGCGGGCTTCCCAAAAAGAGAGAAAGCTCTTCCCA	1192
Qy	1200	CATTAAAGACCTTAACCTTCTTAACAAGACATCCCTGATGAGTCTTTTGTGTGATGTGACA	1259
Db	1193	CATTAAAGACCTTAACCTTCTTAACAAGACATCCCTGATGAGTCTTTTGTGTGATGTGACA	1252
Qy	1260	TGTACAAGCTCTCTGTGAAGACCTTGACAGCTGACTGTTTGCTGCAAGACTTCAAGA	1319
Db	1253	TGTACAAGCTCTCTGTGAAGACCTTGACAGCTGACTGTTTGCTGCTGCAAGACTTCAAGA	1312
Qy	1320	TATATGATTACAGCCCTCTGTAAGTCAATCCATATATATGATCATGACAACAAGAGCCCT	1379
Db	1313	TATATGATTATTAAGCTCTGTAAGTCAATCCATATATATGATCATGACAACAAGAGCCCT	1372
Qy	1380	TAAAGCATGAAACACAGTACTCAGTTGATCTGAAAGACCGGCCCCCAAAAGGCTGTGT	1439
Db	1373	TAAAGCATGAAACACAGTACTCAGTTGATCTGAAAGACCGGCCCCCAAAAGGCTGTGT	1432
Qy	1440	ATTCCAAGCCATGGAATTCATTCACAGGAGAGGCTGAGGGGTGGTACATAGAGAACGTG	1499
Db	1433	ATTCCAAGCCATGGAATTCATTCACAGGAGAGGCTGAGGGGTGGTACATAGAGAACGTG	1492
Qy	1500	ATGACCATATGGGTGTCATCCCTGCCGGAATGTAAGAGGGAAGAGCTTGTCTTATATA	1559
Db	1493	ATGACCATATGGGTGTCATCCCTGCCGGAATGTAAGAGGGAAGAGCTTGTCTTATATA	1552
Qy	1560	TTGGCATCATTTGACATTTCTACAGTCTTTACAGTTTGTTAAGAAAGTTGAGACACTCTGGA	1619
Db	1553	TTGGCATCATTTGACATTTCTACAGTCTTTACAGTTTGTTAAGAAAGTTGAGACACTCTGGA	1612
Qy	1620	AAGCCCTGGATACATGACAGGAGACACTGTCTCAGTGCATGCCCCAGGCTTCTACGCTGAAC	1679
Db	1613	AAGCCCTGGATACATGACAGGAGACACTGTCTCAGTGCATGCCCCAGGCTTCTACGCTGAAC	1672
Qy	1680	GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAAGTTCCCTTGAAGCTTCTCTCTT	1739
Db	1673	GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAAGTTCCCTTGAAGCTTCTCTCTT	1732
Qy	1740	CCAAAAGTTTGGTCTGGCTGCTCATCTTCTCTGGGAGAGAGGCTCAGAGGCAACCTCT	1799
Db	1733	CCAAAAGTTTGGTCTGGCTGCTCATCTTCTCTGGGAGAGAGGCTCAGAGGCAACCTCTCT	1792
Qy	1800	GCATTAATTACAGCCATCGGTCTCTGGGGAACAACAAGGCAACAAGTGACAACAAGGCGAG	1859
Db	1793	GCATTAATTACAGCCATCGGTCTCTGGGGAACAACAAGGCAACAAGTGACAACAAGGCGAG	1852
Qy	1860	AAGTGAAGCCAGGGGTTCACCTTGTGTGTCTGTATGTTTTTAACCTCACAACCTCAACTTTGG	1919
Db	1853	AAGTGAAGCCAGGGGTTCACCTTGTGTGTCTGTATGTTTTTAACCTCACAACCTCAACTTTGG	1912
Qy	1920	AGGAAATCAGTGAAGGGCTCGCTATTTCTGTCAACCCAGTTTCTCACTCTATGTTGAGAGA	1979
Db	1913	AGGAAATCAGTGAAGGGCTCGCTATTTCTGTCAACCCAGTTTCTCACTCTGTTGAGAGA	1972
Qy	1980	CTTTGCAAAATCTTAACATCAAGTACAAACCTTGGAAAAAGCTTGAAGTTGACAGATCAGAT	2039
Db	1973	CTTTGCAAAATCTTAACATCAAGTACAAACCTTGGAAAAAGCTTGAAGTTGACAGATCAGAT	2032
Qy	2040	TCACCCATTAAGCCCAAAAGCTCAGAAAGCTGGAACAAGATTTCTGCATCTCTGTGATC	2099
Db	2033	TCACCCATTAAGCCCAAAAGCTCAGAAAGCTGGAACAAGATTTCTGCATCTCTGTGATC	2092
Qy	2100	CCAAAGTGTACAGCCCTTGCCCCCAGCAATGTCTGAATTTTCTTCTACTTGGTCAATCAAAAA	2159
Db	2093	CCAAAGTGTGTACAGCCCTTGCCCCCAGCAATGTCTGAATTTTCTTCTACTTGGTCAATCAAAAA	2152
Qy	2160	GAAGTGTAAATGAAGTGAAGGGAGGTGTCCTGCAATCTTCTTCTGAAAGAAAGAACTTCT	2219
Db	2153	GAAGTGTAAATGAAGTGAAGGGAGGTGTCCTGCAATCTTCTTCTGAAAGAAAGAACTTCT	2212

Qy	2220	CTCTTCCTCTCCCTCCATGAAATGGGCGCTTAGTGCTCTCAGAGATGTGAGGACCGCAGCATC	2279
Db	2213	CTCTTCCTCTCTCTCAATGAATGGGCTTAGTGCTCTCAGAGATGTGAGGACCGCAGCATC	2272
Qy	2280	CCCTCCACCTCCAGAGTGGGTGGTAACGGATTTTCAACTGGCGAACCTTTGCTCTCACTA	2339
Db	2273	CCCTCCACCTCCAGAGTGGGTGGTAACGGATTTTCAACTGGCGAACCTTTGCTCTCACTA	2332
Qy	2340	TTGAAATTTTTTCAAGCCCGCATTCCTTCAATGCTGGAAATGGGATGCTGAACTTGGCAGC	2399
Db	2333	TTGAAATTTTTTCAAGCCCGCATTCCTTCAATGCTGGAAATGGGATGCTGAACTTGGCAGC	2392
Qy	2400	TTTCTTTCCCTGCTCTTTGACTAGAAACCGGACTCTTAAATTTCTCAGAGACGACTAC	2459
Db	2393	TTTCTTTCCCTGCTCTTTGACTAGAAACCGGACTCTTAAATTTCTCAGAGACGACTAC	2452
Qy	2460	TGGCACTTATTCCTTACTTAATTTCTCTCTGACTCTCTGGAAATATTCCTGTAT	2519
Db	2453	TGGCACTTATTCCTTACTTAATTTCTCTCTGACTCTCTGGAAATATTCCTGTAT	2512
Qy	2520	CTCTGTAAGGTTTTGGGGGATAAGGGTGTAAACACCTCCAGGCTTCTTCTTC	2578
Db	2513	CTCTGTAAGGTTTTGGGGGATAAGGGTGTAAACACCTCCAGGCTTCTTCTTC	2572
Qy	2579	TTTTTTTTCTGAAAAAAGAAAAAGCAACACACACATTTCAAGCATTTTCAATCA	2638
Db	2573	TTTTTTTTCTGAAAAAAGAAAAAGCAACACACACATTTCAAGCATTTTCAATCA	2632
Qy	2659	GAACTCCAGAAAGTTTGACAAAGTCCTATTGTAAGTTCCCTCAGAAAGCATGATG	2698
Db	2653	GAACTCCAGAAAGTTTGACAAAGTCCTATTGTAAGTTCCCTCAGAAAGCATGATG	2692
Qy	2699	TTTATGAAGAAGAGTAGTATGTGCTCTGCGAAGACGCTCTTTTAACTCTCTCT	2758
Db	2693	TTTATGAAGAAGAGTAGTATGTGCTCTGCGAAGACGCTCTCTTTTAACTCTCTCT	2752
Qy	2759	CTCTTGATGAATTTCTTAAAGCTGGAAGAAATGAAGAATGGGATATCTTAA	2818
Db	2753	CTCTTGATGAATTTCTTAAAGCTGGAAGAAATGAAGAATGGGATATCTTAA	2812
Qy	2819	TCCCTTTGTTAAAAACAGAGGACGACATAGGGCTGGAGATCATAGCCCTTCTAGGAC	2878
Db	2813	TCCCTTTGTTAAAAACAGAGGACGACATAGGGCTGGAGATCATAGCCCTTCTAGGAC	2872
Qy	2879	AATCTGTTCACTGCGAGGCTATAGTAATTAATTAATTTTGGCAATTTGAAATATATCT	2938
Db	2873	AATCTGTTCACTGCGAGGCTATAGTAATTAATTAATTTTGGCAATTTGAAATATATCT	2932
Qy	2939	GCTTGTTTTCTAAATGTGAAGCTTACCAAAATGAATTTTAGATCATTCTCCAGAGGA	2998
Db	2933	GCTTGTTTTCTAAATGTGAAGCTTACCAAAATGAATTTTAGATCATTCTCCAGAGGA	2992
Qy	2999	TTTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTCTCTGTTTTGTGAAGCTAAGGTAA	3058
Db	2993	TTTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTCTCTGTTTTGTGAAGCTAAGGTAA	3052
Qy	3059	GAGGGGACATTCGTGCTGTTTTAACAAGACATATCTGTGAAGGCGACAGAAATATTTT	3118
Db	3053	GAGGGGACATTCGTGCTGTTTTAACAAGACATATCTGTGAAGGCGACAGAAATATTTT	3112
Qy	3119	CTTAAACTCATGGGAGACAGACAGATTCCTTGCTGGTAGGTCAATGCTGTGCATATG	3178
Db	3113	CTTAAACTCATGGGAGACAGACAGATTCCTTGCTGGTAGGTCAATGCTGTGCATATG	3172
Qy	3179	TCTTAACCCCTGTCTTTCATGTCAGGGAAATTTGGAATTTGGGGCTCAATAGCCCTCT	3238
Db	3173	TCTTAACCCCTGTCTTTCATGTCAGGGAAATTTGGAATTTGGGGCTCAATAGCCCTCT	3232
Qy	3239	CCCCGCTACAAAGATGTGGTTTTTTCATCTGAATCTTCCACTCTGTCTCAGGGGAAGAG	3298
Db	3233	CCCCGCTACAAAGATGTGGTTTTTTCATCTGAATCTTCCACTCTGTCTCAGGGGAAGAG	3292

QY 3299 GGGGCTGGATCTCAGCAGATGTTGAATTCCTGTTCTATCCCTCTCTATCCACC 3358
Db 3293 GGGGCTGGATCTCAGCAGATGTTGAATTCCTGTTCTATCCCTCTCTATCCACC 3352
QY 3359 TGGCTTGAATTAATGTTAGCCCATACCCCAATTAATGTTATTAAGACACCCCAACC 3418
Db 3353 TGGCTTGAATTAATGTTAGCCCATACCCCAATTAATGTTATTAAGACACCCCAACC 3412
QY 3419 AGTTCTGGCTGCTGCTGTTGCTGCATGTTTCTTAACAAGAAAGAAATCTTGCTA 3478
Db 3413 AGTTCTGGCTGCTGCTGTTGCTGCATGTTTCTTAACAAGAAAGAAATCTTGCTA 3472
QY 3479 TTTTCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3538
Db 3473 TTTTCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3532
QY 3539 TGTTAGGGGTGGAGGAAATTTTGAAGAGGGCTGGCTTTAGGAAAGAAATGGGAA 3598
Db 3533 TGTTAGGGGTGGAGGAAATTTTGAAGAGGGCTGGCTTTAGGAAAGAAATGGGAA 3592
QY 3599 GCAACATTTTATTAAGTTACTATTTGCTCTACTATTTGCTCTATTTGTTGCAAAATGGCAA 3658
Db 3593 GCAACATTTTATTAAGTTACTATTTGCTCTACTATTTGCTCTATTTGTTGCAAAATGGCAA 3652
QY 3659 TACATATTAAGTATATATGTTTATTAATTAATTAATTAATTAATTAATTAATTA 3713
Db 3653 TACATATTAAGTATATATGTTTATTAATTAATTAATTAATTAATTAATTAATTA 3707

RESULT 5
US-60-453-135-2839
; Sequence 2839, Application US/60453135
; GENERAL INFORMATION:
; APPLICANT: CARBIL, Michele
; APPLICANT: IAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CI001456
; CURRENT APPLICATION NUMBER: US/60/453.135
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2839
; LENGTH: 3707
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-453-135-2839

Query Match 96.3%; Score 3575.8; DB 11; Length 3707;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 3660; Conservative 3; Mismatches 15; Indels 37; Gaps 4;

QY 1 ATTAACAGGCGGTGTAAGAAAGCGAAGAGGGCGTTGCTCTTTGGACCTTTCA 60
Db 28 ATTAACAGGCGGTGTAAGAAAGCGAAGAGGGCGTTGCTCTTTGGACCTTTCA 87
QY 61 TGGCTGTTTCTTTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
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RESULT 7
 US-09-724-676-21450
 ; Sequence 21450, Application US/09724676
 ; GENERAL INFORMATION:
 ; APPLICANT: Compugen LTD
 ; TITLE OF INVENTION: Variants of alternative splicing
 ; FILE REFERENCE: 129181.4 Compugen
 ; CURRENT APPLICATION NUMBER: US/09/724,676
 ; NUMBER OF SEQ ID NOS: 2000-11-28
 ; SOFTWARE: Patentin version 3.2

SEQ ID NO 21450
LENGTH: 3586
TYPE: DNA
ORGANISM: Homo sapiens
US-09-724-676-21450

Query Match 84.2%; Score 3125; DB 6; Length 3586;
Best Local Similarity 92.5%; Pred. No. 0;
Matches 3435; Conservative 0; Mismatches 0; Indels 280; Gaps 3;

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DB 1718 GGTTCAGGCGCTTCAATGTGCAACACAGATTTAAGAAATCCCTGAAAGGCTTCTCCTT 1777
QY 1740 CCAAAAAGTTTCGGTCTGAGCTCATCTTCTCTCGGCGAGAGGCTTCCAGTGGCACTCT 1799
DB 1778 CCAAAAAGTTTCGGTCTGAGCTCATCTTCTCTCGGCGAGAGGCTTCCAGTGGCACTCT 1837
QY 1800 GCATTACTTACCAAGCATCGGTCTCTGAGGAAACAAGGCAAGAGTGCACAAAGGAG 1859
DB 1838 GCATTACTTACCAAGCATCGGTCTCTGAGGAAACAAGGCAAGAGTGCACAAAGGAG 1897
QY 1860 AAGTGAAGCAGGCGTTCACCTTGTGTCTGTATGTTTAACTCAAGCTCACCTTGG 1919
DB 1898 AAGTGAAGCAGGCGTTCACCTTGTGTCTGTATGTTTAACTCAAGCTCACCTTGG 1957
QY 1920 AGGAATCAGTGAAGGCTCGCTATTCCTGACCCCAAGTTTCTCACTCTATGTTGAGAGA 1979
DB 1958 AGGAATCAGTGAAGGCTCGCTATTCCTGACCCCAAGTTTCTCACTCTATGTTGAGAGA 2017
QY 1980 CTTTGCAATGCTTAACTTCAAGTACAACTTGTGAAAAGCTTGAAGTGTGACAGTCAAGT 2039
DB 2018 CTTTGCAATGCTTAACTTCAAGTACAACTTGTGAAAAGCTTGAAGTGTGACAGTCAAGT 2077

QY 2040 TCACCATTAAGCGAAGCCTCAGAGACCTGGAACAAGATTCGCACTGTGTATC 2099
 DB 2078 TCACCATTAAGCGAAGCCTCAGAGACCTGGAACAAGATTCGCACTGTGTATC 2137
 QY 2100 CCAAGATGTAGAGCCCTGCGCCAGCAATGCTGAATTTTCTTCTATCTGTATCAAAAAA 2159
 DB 2138 CCAAGATGTAGAGCCCTGCGCCAGCAATGCTGAATTTTCTTCTATCTGTATCAAAAAA 2197
 QY 2160 GAGGTGTATAGATGAGGGAGAGCTGCTCCCTCAATCTTCTTCTGGAAGAAACCTTCT 2219
 DB 2198 GAGGTGTATAGATGAGGGAGAGCTGCTCCCTCAATCTTCTTCTGGAAGAAACCTTCT 2257
 QY 2220 CTCCTCCCTCTCTCATGAAATGAGGCTTAGAGCTCAGAGAGTGAAGAGACGAGCATC 2279
 DB 2258 CTCCTCCCTCTCTCATGAAATGAGGCTTAGAGCTCAGAGAGTGAAGAGACGAGCATC 2317
 QY 2280 CCCTCCTCCTCAGAGTGTGGGTGTAGAGATTTTCAACTGCGCAACCTTTGCTCCACTA 2339
 DB 2318 CCCTCCTCCTCAGAGTGTGGGTGTAGAGATTTTCAACTGCGCAACCTTTGCTCCACTA 2377
 QY 2340 TTGAATTTTTCAGACCCCACTTCTTCATGCTGGAATGGAATGCTGGAATGCTGGAAC 2399
 DB 2378 TTGAATTTTTCAGACCCCACTTCTTCATGCTGGAATGGAATGCTGGAATGCTGGAAC 2437
 QY 2400 TTTCTTTCCCTGCTGTGTAGACTAGAGACCGGACTTTAATTTCTCAGAGACAGACTAGC 2459
 DB 2438 TTTCTTTCCCTGCTGTGTAGACTAGAGACCGGACTTTAATTTCTCAGAGACAGACTAGC 2497
 QY 2460 TGGCACAATTAATCCCTAAGTTAGTTCTTCTCTGACCTCTGGAAGATATGCTGTAT 2519
 DB 2498 TGGCACAATTAATCCCTAAGTTAGTTCTTCTCTGACCTCTGGAAGATATGCTGTAT 2557
 QY 2520 CTCCTGAAGCTTTTGGGGAGTAAGGGGTGTAACACCTCCAGCTTCTTCTC-TT 2578
 DB 2558 CTCCTGAAGCTTTTGGGGAGTAAGGGGTGTAACACCTCCAGCTTCTTCTC-TT 2617
 QY 2579 TTTTCTTCTGAAGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGG 2638
 DB 2618 TTTTCTTCTGAAGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGG 2677
 QY 2639 GAACTCCAGAGTGTGTAGCAAGATGCTTATGCTGTAGATTTCTCTGAAAGGCAATGCTG 2698
 DB 2678 GAACTCCAGAGTGTGTAGCAAGATGCTTATGCTGTAGATTTCTCTGAAAGGCAATGCTG 2737
 QY 2699 TTTATGAAGAGAGAGATGATGCTGCTGCGAGAGAGAGCTCTCTTAAATCTCTCT 2758
 DB 2738 TTTATGAAGAGAGAGATGATGCTGCTGCGAGAGAGAGCTCTCTTAAATCTCTCT 2797
 QY 2759 CTGTGTATGAAATTTCTTAAGGCTGAAGATGAAGAGATGAGGAGATGAGGATCTTTA 2818
 DB 2798 CTGTGTATGAAATTTCTTAAGGCTGAAGATGAAGAGATGAGGAGATGAGGATCTTTA 2857
 QY 2819 TCCCTTTTGTAAAG 2878
 DB 2858 TCCCTTTTGTAAAG 2917
 QY 2879 AATCCGTTACGTCGAG 2938
 DB 2918 AATCCGTTACGTCGAG 2977
 QY 2939 GGTGTGTGTCTAATGTGAAGATTAACAATGAATTTTATGATCTTCCAGAGAGAGAGAG 2998
 DB 2978 GGTGTGTGTCTAATGTGAAGATTAACAATGAATTTTATGATCTTCCAGAGAGAGAGAG 3037
 QY 2999 TTTTGTGTGTCTCTCTCATCTTTTCCAAAGGTGCTCTGTTGTGAGACTGAAGGTAAG 3058
 DB 3038 TTTTGTGTGTCTCTCTCATCTTTTCCAAAGGTGCTCTGTTGTGAGACTGAAGGTAAG 3097
 QY 3059 GAGGGAGACATCTGTCTGTGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3118
 DB 3098 GAGGGAGACATCTGTCTGTGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3147
 QY 3119 CTTAAATCATGTGGAGAGAGAGAGATTTGCTGTGTGAGGTCAATGCTGTGTGATATG 3178

DB 3148 ----- 3147
 QY 3179 TCCATCCCCCTGTCTTCAATGAGGAGAGTGGAAATGGGGGCTACATATGCCCCCTCT 3238
 DB 3148 ----- 3147
 QY 3239 CCCGCTACAGAGTGTGTGTTTCCATCTGATCTCTTCACTTGTGTGAGGGAGAGAG 3298
 DB 3148 ----- 3147
 QY 3299 GGGGCTGTATCTCAGAGAGATTTGTAATTCCTGTCTATCTCTATCCACCC 3358
 DB 3148 ----- 3147
 QY 3359 TGCCTGTATATATGTAGCCCATACCCCAATTAATGCTATATATAGACACCCCGAGCC 3418
 DB 3148 ----- 3147
 QY 3419 AGTTCTGCTGCTGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3478
 DB 3180 AGTTCTGCTGCTGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3539
 QY 3479 TTTTCTTCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3538
 DB 3240 TTTTCTTCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3599
 QY 3539 TGTAGGGGAGGAGGAGATTTTGAAGAGAGGCTGGCTTTAGGAGAGAGAGAGAGAGAG 3598
 DB 3300 TGTAGGGGAGGAGGAGATTTTGAAGAGAGGCTGGCTTTAGGAGAGAGAGAGAGAGAG 3559
 QY 3599 GCAACATTTTATTAAGTGTACTTATTTGCTCTACTTGTATTTTCAAGAAATGCGAAA 3658
 DB 3360 GCAACATTTTATTAAGTGTACTTATTTGCTCTACTTGTATTTTCAAGAAATGCGAAA 3419
 QY 3659 TACAATATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3713
 DB 3420 TACAATATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3474

RESULT 8
 US-09-724-676A-21450
 ; Sequence 21450, Application US/09724676A

; GENERAL INFORMATION:
 ; APPLICANT: Comugen LTD
 ; TITLE OF INVENTION: Variants of alternative splicing
 ; FILE REFERENCE: 129181.4 Comugen
 ; CURRENT APPLICATION NUMBER: US/09/724,676A
 ; CURRENT FILING DATE: 2000-11-28
 ; NUMBER OF SEQ ID NOS: 97222
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 21450
 ; LENGTH: 3586
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

US-09-724-676A-21450

Query Match 84.2%; Score 3125; DB 6; Length 3586;
 Best Local Similarity 92.5%; Pred. No. 0;
 Matches 3435; Conservative 0; Mismatches 0; Indels 280; Gaps 3;

QY 1 ATTAACAGGCGGTGTATGAAG 60
 DB 38 ATTAACAGGCGGTGTATGAAG 97
 QY 61 TGCCTGCTTTTTCAGATGTGCTGTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
 DB 98 TGCCTGCTTTTTCAGATGTGCTGTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 157
 QY 121 AGCTTACTCTTCTGTGAAG 180
 DB 158 AGCTTACTCTTCTGTGAAG 217

Qy 181 GGGGTGCGGAGCGTGAAGTTCTTCCCATGCCAGCGAAAGTGTTGGCTTGAAGTGTCTC 240
Db 218 GGGGTGCGGAGCGTGAAGTTCTTCCCATGCCAGCGAAAGTGTTGGCTTGAAGTGTCTC 277
Qy 241 AGGAGCCGGCTCGAGCTGTCTGAAGGAGG-CCCGAGGGGGCGGGAGGTGGCCCAAGA 299
Db 278 AGGAGCCGGCTCGAGCTGTCTGAAGGAGGCGCCGAGGGGGCGGGAGGTGGCCCAAGA 337
Qy 300 AGCGGGTTCTGTAAAGAGCGTTGGGAAGATTGATTCCGAGAAAGAGAAAGAACCGGAT 359
Db 338 AGCGGGTTCTGTAAAGAGCGTTGGGAAGATTGATTCCGAGAAAGAGAAAGAACCGGAT 397
Qy 360 TGAAGAGAGCGAGCGCTGAGGGGGAGGGGGCTCTTAAGATGCGTCCGCTCTCCG 419
Db 398 TGAAGAGAGCGAGCGCTGAGGGGGAGGGGGCTCTTAAGATGCGTCCGCTCTCCG 457
Qy 420 GGGCGTGTCTTCCGTCGGTCTTCTTATCTTGAATCCCGCGGTCCCTTCTGTATCTTGT 479
Db 458 GGGCGTGTCTTCCGTCGGTCTTCTTATCTTGAATCCCGCGGTCCCTTCTGTATCTTGT 517
Qy 480 CCTGAGCATCTGGAATCAAGAGACCATAGGCACTGAGGTGCTTAAGCTCTGCGCATGC 539
Db 518 CCTGAGCATCTGGAATCAAGAGACCATAGGCACTGAGGTGCTTAAGCTCTGCGCATGC 577
Qy 540 CCATCAAGAAATAGGCCATAGAGTGTGAATCTCTGAGAGAGACAATATATAAAGA 599
Db 578 CCATCAAGAAATAGGCCATAGAGTGTGAATCTCTGAGAGAGACAATATATAAAGA 637
Qy 600 CAACCTCATGAGCTTGAAGAGTGCATTCAGTTAGGCAATACCAACTGTGGGAGCC 659
Db 638 CAACCTCATGAGCTTGAAGAGTGCATTCAGTTAGGCAATACCAACTGTGGGAGCC 697
Qy 660 TGAGTACCAACAGAGGAGTATGCTCATAGCAAGATTCTACGTGTGAGAGATATCT 719
Db 698 TGAGTACCAACAGAGGAGTATGCTCATAGCAAGATTCTACGTGTGAGAGATATCT 757
Qy 720 TCTTCCAGTGAAGGAGCAACTGACCCCTGCTCATCACTACATGACTTTCGTTCA 779
Db 758 TCTTCCAGTGAAGGAGCAACTGACCCCTGCTCATCACTACATGACTTTCGTTCA 817
Qy 780 AGACCTATGCACTGTGCTTCCGCTTCCGCTTCCGAGAGCTATTTGGTATCCGGCCGATG 839
Db 818 AGACCTATGCACTGTGCTTCCGCTTCCGCTTCCGAGAGCTATTTGGTATCCGGCCGATG 877
Qy 840 ATTACTGTATTCCTCTGCACTGAGCGCGTGAATGAATCTGTAGCTCTGAGAGTATG 899
Db 878 ATTACTGTATTCCTCTGCACTGAGCGCGTGAATGAATCTGTAGCTCTGAGAGTATG 937
Qy 900 GTTCCCTATTTATGTGTCTGAGCGAGATGATGATTAATTATGACATCCAACTAAG 959
Db 938 GTTCCCTATTTATGTGTCTGAGCGAGATGATGATTAATTATGACATCCAACTAAG 997
Qy 960 AGGGGAAATTTCTGCAAGAGCTGCTTCAAGATTAATGATGAACCTCAACAGAACCTC 1019
Db 998 AGGGGAAATTTCTGCAAGAGCTGCTTCAAGATTAATGATGAACCTCAACAGAACCTC 1057
Qy 1020 GGAATTTGCTGCTAAATTTCTATGAGACTGTATCTGTGTGCAAGCGAGTGTGCAAGATTC 1079
Db 1058 GGAATTTGCTGCTAAATTTCTATGAGACTGTATCTGTGTGCAAGCGAGTGTGCAAGATTC 1117
Qy 1080 GGAATTTGCTGATGAACAATCTTTTACCAAGATCGTAAATAATGATATCAATATGAC 1139
Db 1118 GGAATTTGCTGATGAACAATCTTTTACCAAGATCGTAAATAATGATATCAATATGAC 1177
Qy 1140 TCAAAAGCTCAACCTTAACAACGCGCGGCTTCCAGAAAGAGGAGAGAGCTCTTCCA 1199
Db 1178 TCAAAAGCTCAACCTTAACAACGCGCGGCTTCCAGAAAGAGGAGAGAGCTCTTCCA 1237
Qy 1200 CATTTAAAGACTGAGACTTTTATGAAGAATCCCTGATGAGTCTTTTGTGATGCTGACA 1259
Db 1238 CATTTAAAGACTGAGACTTTTATGAAGAATCCCTGATGAGTCTTTTGTGATGCTGACA 1297
Qy 1260 TGTACAAGCTCTCTGTAGAAGCCTGCAAGCGTGAAGTGTGGTGTGAGAGCTTCAAGA 1319

Db 1298 TGTACAAGCTCTCTGTAGAAGCCTGCAAGCGTGAAGTGTGGTGTGCTGAGAGCTTCAAGA 1357
Qy 1320 TAAATGATTAAGCTCTTGAATGTCAATCCATATATATGATCATGACAAAGAGCCCT 1379
Db 1358 TAAATGATTAAGCTCTTGAATGTCAATCCATATATATGATCATGACAAAGAGCCCT 1417
Qy 1380 TAAAGATGAACAAGTATCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1439
Db 1418 TAAAGATGAACAAGTATCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1477
Qy 1440 ATTCAAGCCATGAAATCCATCCAGGAGAGGCTCGACGGGGTGTATCAATGAGACTG 1499
Db 1478 ATTCAAGCCATGAAATCCATCCAGGAGAGGCTCGACGGGGTGTATCAATGAGACTG 1537
Qy 1500 ATGACATATAGGTGGGCAATCCCTGCGCGGAATAGTAAAGGGGAAAGCTTCTCTTATA 1559
Db 1538 ATGACATATAGGTGGGCAATCCCTGCGCGGAATAGTAAAGGGGAAAGCTTCTCTTATA 1597
Qy 1560 TTGGCATCATGACATTTCTACAGTCTTACAGGTTTGTAAAGAGTTGAGAGACTCTTGA 1619
Db 1598 TTGGCATCATGACATTTCTACAGTCTTACAGGTTTGTAAAGAGTTGAGAGACTCTTGA 1657
Qy 1620 AAGCCCTGTATCATGACGAGAGACATGCTCTCAATGATGATGATGATGATGATGATGATGAT 1679
Db 1658 AAGCCCTGTATCATGACGAGAGACATGCTCTCAATGATGATGATGATGATGATGATGATGAT 1717
Qy 1680 GGTTCAGCGCTTATGTGCAACAGTATTAAGAAAGTTCCCTTGAAGCTTCTCTT 1739
Db 1718 GGTTCAGCGCTTATGTGCAACAGTATTAAGAAAGTTCCCTTGAAGCTTCTCTT 1777
Qy 1740 CCAAAAGTTTGGTGGGCTCATCTTCTCTGCGAGAGCGCTCCAGTGGCAATCCT 1799
Db 1778 CCAAAAGTTTGGTGGGCTCATCTTCTCTGCGAGAGCGCTCCAGTGGCAATCCT 1837
Qy 1800 GCATTACTTACAGCACTGCTCTCTGCGGAAACAAGGCAACAAGTACAAAGAGCAG 1859
Db 1838 GCATTACTTACAGCACTGCTCTCTGCGGAAACAAGGCAACAAGTACAAAGAGCAG 1897
Qy 1860 AAGTGAAGCCAGGCGTTCACTTGTGTCTGTATGTTTAACTCAAGCTTCACTTGTG 1919
Db 1898 AAGTGAAGCCAGGCGTTCACTTGTGTCTGTATGTTTAACTCAAGCTTCACTTGTG 1957
Qy 1920 AGGAAATCAGTGAAGGCGCTGCTATGCTGACCCAGTTTCTCACTTGTGAGAGA 1979
Db 1958 AGGAAATCAGTGAAGGCGCTGCTATGCTGACCCAGTTTCTCACTTGTGAGAGA 2017
Qy 1980 CTTTGCAATGCTAATCAAGTACAACTTGAAGAGTTGAAGTTGAGAGTCAAGT 2039
Db 2018 CTTTGCAATGCTAATCAAGTACAACTTGAAGAGTTGAAGTTGAGAGTCAAGT 2077
Qy 2040 TCACCATTAAGCGCAAGCTCAGAAAGCTGGAACAAGATTTCTGCAATCTGTGATC 2099
Db 2078 TCACCATTAAGCGCAAGCTCAGAAAGCTGGAACAAGATTTCTGCAATCTGTGATC 2137
Qy 2100 CCAAGATGACGCGCTGCGCCAGCAATGCTGAATTTCTTCTTCACTGATCAATAAAA 2159
Db 2138 CCAAGATGACGCGCTGCGCCAGCAATGCTGAATTTCTTCTTCACTGATCAATAAAA 2197
Qy 2160 GGAATGTAATGAAGTGAAGGAGCTGCTCTCATCTTCTTCTGAAAGAAAGCTTCT 2219
Db 2198 GGAATGTAATGAAGTGAAGGAGCTGCTCTCATCTTCTTCTGAAAGAAAGCTTCT 2257
Qy 2220 CTCCTTCTCTTCTCATGAATGAGGCTTATGCTCTGAGAGATTTGAGAGCGAGCATC 2279
Db 2258 CTCCTTCTCTTCTCATGAATGAGGCTTATGCTCTGAGAGATTTGAGAGCGAGCATC 2317
Qy 2280 CCGTCCACTCAGAGTGGGAGTGAAGGATTTTCACTGCGCAACCTTGGCCCTCCACTA 2339
Db 2318 CCGTCCACTCAGAGTGGGAGTGAAGGATTTTCACTGCGCAACCTTGGCCCTCCACTA 2377
Qy 2340 TTGAATTTTTTCAAGCCCATCTTCACTGCTGAAGATGAGATTTGCTGAGCTTGGAGC 2399

Db 2378 TTGAATTTTTCAGACCCCAATCTTCATGCTGAGAAATGGGATTGCTGGACTGGACG 2437
 Qy 2400 TTTCTTTCCCTCGTCTTTGATGAGAACCGGACTTTAATTTCTCGAGACAGACTAGC 2459
 Db 2438 TTTCTTTCCCTCGTCTTTGATGAGAACCGGACTTTAATTTCTCGAGACAGACTAGC 2497
 Qy 2460 TGGCAGATTATCCCTCACTTATGTTCTTTCTCTGATCCTCCGAGAAATATCTCCGTAT 2519
 Db 2498 TGGCAGATTATCCCTCACTTATGTTCTTTCTCTGATCCTCCGAGAAATATCTCCGTAT 2557
 Qy 2520 CTCTGTAAGGTTTGGGGGATAAGGTTTAAACAACCTCCAGCTTCTCTTC- TT 2578
 Db 2558 CTCTGTAAGGTTTGGGGGATAAGGTTTAAACAACCTCCAGCTTCTCTTC- TT 2617
 Qy 2579 TTTTCTTCTGAAAAAGAAAAAGCAACAGACACATTTCAAGCCATTTTCAGATCA 2638
 Db 2618 TTTTCTTCTGAAAAAGAAAAAGCAACAGACACATTTCAAGCCATTTTCAGATCA 2677
 Qy 2639 GAACCTCCAGAAAGTGTGACAAATGCTATTTGTAGATTCTCCAGAAAGCCATGGTG 2698
 Db 2678 GAACCTCCAGAAAGTGTGACAAATGCTATTTGTAGATTCTCCAGAAAGCCATGGTG 2737
 Qy 2699 TTTATGAAGAAGAGTATGCTCTGCGAAGAGAGCTCTCTTTAAACTCTCTCT 2758
 Db 2738 TTTATGAAGAAGAGTATGCTCTGCGAAGAGAGCTCTCTTTAAACTCTCTCTCT 2797
 Qy 2759 CTCTTGATGATTTCTTAAAGCTGAAAGATGAAGAGTGGGACATGGGGTAACTTTA 2818
 Db 2798 CTCTTGATGATTTCTTAAAGCTGAAAGATGAAGAGTGGGACATGGGGTAACTTTA 2857
 Qy 2819 TCCCTTTGTAAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2878
 Db 2858 TCCCTTTGTAAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2917
 Qy 2879 AATCTGTTCACTGCGAGGCTATAGTAATTAATTAATTTTCAATTTGAAATATATCT 2938
 Db 2918 AATCTGTTCACTGCGAGGCTATAGTAATTAATTAATTTTCAATTTGAAATATATCT 2977
 Qy 2939 GGTGTTTCTTAATGTGAAGCTTAACCAATTTTAATGATCACTTCCAGAGAGA 2998
 Db 2978 GGTGTTTCTTAATGTGAAGCTTAACCAATTTTAATGATCACTTCCAGAGAGA 3037
 Qy 2999 TTTTCTTCTCTCTCATCTTTTCAAGAGGTTCTCCGTTTGGAGCTAAGTAA 3058
 Db 3038 TTTTCTTCTCTCTCATCTTTTCAAGAGGTTCTCCGTTTGGAGCTAAGTAA 3097
 Qy 3059 GAGGGAGCACTTCTGCTGTTTAAAGAGAGTCAATATCTGAGGCGAGCAAAATTTT 3118
 Db 3098 GAGGGAGCACTTCTGCTGTTTAAAGAGAGTCAATATCTGAGGCGAG----- 3147
 Qy 3119 CTTAACTCATGGGAGAGAGAGATTTGCTTGAGAGTCACTTGCTGAGCATATG 3178
 Db 3148 ----- 3147
 Qy 3179 TCTTACCCCTGCTTTCATGACAGGAAATGGGGCTATATGCCCCCTCTCTCT 3238
 Db 3148 ----- 3147
 Qy 3239 CCCCCTCAAGAGTTGGTTTCCATCTGATCCTTCACTTTGTCAGGGGAAAGAA 3298
 Db 3148 ----- 3147
 Qy 3299 GGGGCTGATCTCAGGAGAGATTTGAAATCTCTGTTCTATCCCTCTCTATCCACCC 3358
 Db 3148 ----- 3147
 Qy 3359 TGCCTTATATATGTTAGCCCATACCCCAATATGTTATATTAAGACACCCAGCC 3418
 Db 3148 -----CAATATATGTTATATTAAGACACCCAGCC 3179
 Qy 3419 AGTTTCTGGCTGCTGCTTTTGTGTCAGATTTTAAAGAAAGAAAGATTTGCTA 3478
 Db 3180 AGTTTCTGGCTGCTGCTTTTGTGTCAGATTTTAAAGAAAGAAAGATTTGCTA 3539

Qy 3479 TTTTCTTCAATAATTACATTTATGATGATTTAAGTGTATTAAGACAGAGTTC 3538
 Db 3240 TTTTCTTCAATAATTACATTTATGATGATTTAAGTGTATTAAGACAGAGTTC 3299
 Qy 3539 TGTAAAGGAGTGGAGGAAATTTTGAAGAGGAGGCTGGGCTTTAAGGAAAGAAATGGGAA 3598
 Db 3300 TGTAAAGGAGTGGAGGAAATTTTGAAGAGGAGGCTGGGCTTTAAGGAAAGAAATGGGAA 3359
 Qy 3599 GCAACATTTTATTAAGTGTATTTTGGCTTACTTGTATGTTGCAAAATGGCAAA 3658
 Db 3360 GCAACATTTTATTAAGTGTATTTTGGCTTACTTGTATGTTGCAAAATGGCAAA 3419
 Qy 3659 TACAATTAAGGATATATGTTTAAATGTAATAACTTTAATGATTAATTA 3713
 Db 3420 TACAATTAAGGATATATGTTTAAATGTAATAACTTTAATGATTAATTA 3474

 RESULT 9
 US-09-724-676-21453
 ; Sequence 21453, Application US/09724676
 ; GENERAL INFORMATION:
 ; APPLICANT: Compugen LTD
 ; TITLE OF INVENTION: Variants of alternative splicing
 ; FILE REFERENCE: 129181.4 Compugen
 ; CURRENT APPLICATION NUMBER: US/09/724,676
 ; NUMBER OF SEQ ID NOS: 97222
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 21453
 ; LENGTH: 3622
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-724-676-21453

 Query Match 82.3%; Score 3079; DB 6; Length 3622;
 Best Local Similarity 91.6%; Pred. No. 0;
 Matches 3435; Conservative 0; Mismatches 0; Indels 316; Gaps 4;

 Qy 1 ATTAACAGCCCGGTGTTAAGAGACGAGAGAGGGGCTTCGCTTTGGGACTTTTCA 60
 Db 38 ATTAACAGCCCGGTGTTAAGAGACGAGAGAGGGGCTTCGCTTTGGGACTTTTCA 97
 Qy 61 TGCCTGTTTTTTTTCAGATGCGCTTGTCTGCGGCAAGGTCCTCCAGCAGCAGCTTA 120
 Db 98 TGCCTGTTTTTTTTCAGATGCGCTTGTCTGCGGCAAGGTCCTCCAGCAGCAGCTTA 157
 Qy 121 AGCTTACTCTTCTGTGAAGAGGGAAGTATCCCTGTGGAAGAGGGGTTAACTTGAGAG 180
 Db 158 AGCTTACTCTTCTGTGAAGAGGGAAGTATCCCTGTGGAAGAGGGGTTAACTTGAGAG 217
 Qy 181 GGGGTGCGGAGCGTAGATTTTCCCATGCAAGCGAATGCTGTGAGCTTGAGCTGCTC 240
 Db 218 GGGGTGCGGAGCGTAGATTTTCCCATGCAAGCGAATGCTGTGAGCTTGAGCTGCTC 277
 Qy 241 AGAGCCCGGCTGACGTTCTTGAAGAGG-CCCGAGAGGGGCGGAGAGTGGCCCAAGA 299
 Db 278 AGAGCCCGGCTGACGTTCTTGAAGAGG-CCCGAGAGGGGCGGAGAGTGGCCCAAGA 337
 Qy 300 ACGGGGTTCTGTAAAGAGAGTGGGAAGTTGATTCGAGAAAGAGGAACCGGAT 359
 Db 338 ACGGGGTTCTGTAAAGAGAGCGTTGGGAAGTTGATTCGAGAAAGAGGAACCGGAT 397
 Qy 360 TGAAGAAGACAGGCGCTGAGGGGAGGGGCTGTAAGATGCGCTCGGCTCTCCG 419
 Db 398 TGAAGAAGACAGGCGCTGAGGGGAGGGGCTGTAAGATGCGCTCGGCTCTCCG 457
 Qy 420 GGCCTGCTCTTGGTGGGTTTTCATCTTTGATCCCGGCTCTTCTGTAACCTGT 479
 Db 458 GGCCTGCTCTTGGTGGGTTTTCATCTTTGATCCCGGCTCTTCTGTAACCTGT 517
 Qy 480 CCTCAGATCTGGAATCAAGAGACCATGCGATCTGA----- 516

Dh 518 CTTGAGCATCTGGAAATCAAGAGACCATGGCATCTGAGCTCTTGGAGCTAGACAGATT 577
Qy 517 -----GGTGCCTTAGCTCTGGCATGCCCCATCAAGAAATAGGCCATAGAA 563
Dh 578 CTTACATCTCATTTGGTGGCTTAGTGTCTGGCATGCCATCAAGAAATAGGCCATAGAA 637
Qy 564 GTGTGATTTCTCAGAGAGACAACATATATAAAGACAACCTCATACGCTTTGAAAGGTG 623
Dh 638 GTGTGATTTCTCAGAGAGACAACATATATAAAGACAACCTCATACGCTTTGAAAGGTG 697
Qy 624 CCATCCATTTAGGCACTTACCACTGTGGGAGGCTTAGTAACCAACCAAGCTGATG 683
Dh 698 CCATCCATTTAGGCACTTACCACTGTGGGAGGCTTAGTAACCAACCAAGCTGATG 757
Qy 684 TCTCATCTCAAGATTTCTACGCTGTGAGAGATCTTCTTCCAGTAAAGGAGCAAC 743
Dh 758 TCTCATCTCAAGATTTCTACGCTGTGAGAGATCTTCTTCCAGTAAAGGAGCAAC 817
Qy 744 TGACCCCTGCTCATCTACATCAATGACTTTCGTTTCAGACCTATGCACTGTGCTTCC 803
Dh 818 TGACCCCTGCTCATCTACATCAATGACTTTCGTTTCAGACCTATGCACTGTGCTTCC 877
Qy 804 GCTACTTCCGGAGCTATTGGTATCCGCCCCGATGATTACTTGATTCCTCTGCACTG 863
Dh 878 GCTACTTCCGGAGCTATTGGTATCCGCCCCGATGATTACTTGATTCCTCTGCACTG 937
Qy 864 AGCGCTGATTTGAACCTGTAGCTCTGAGAGCTAGTGTTCCTATCTATGTCACAGG 923
Dh 938 AGCGCTGATTTGAACCTGTAGCTCTGAGAGCTAGTGTTCCTATCTATGTCACAGG 997
Qy 924 ACGATGATTTATTAAGAAGTCAACATTAAGAGGCGGAAATTTGCGAGAGCTGC 983
Dh 998 ACGATGATTTATTAAGAAGTCAACATTAAGAGGCGGAAATTTGCGAGAGCTGC 1057
Qy 984 TTCCAGATTTACTAATGAACCTCAACCAAGAACTTCTGCACTTGTGCTTAATTTATG 1043
Dh 1058 TTCCAGATTTACTAATGAACCTCAACCAAGAACTTCTGCACTTGTGCTTAATTTATG 1117
Qy 1044 GACTGTACTGTGTGAGGAGGCTGAGCAAGAACTTGGATTTGTGTGTAACATCTTT 1103
Dh 1118 GACTGTACTGTGTGAGGAGGCTGAGCAAGAACTTGGATTTGTGTGTAACATCTTT 1177
Qy 1104 TACCAAGATTCGTAATAAATGCAATATGACCTCAAGAGCTCAACCTTCAACAGCCG 1163
Dh 1178 TACCAAGATTCGTAATAAATGCAATATGACCTCAAGAGCTCAACCTTCAACAGCCG 1237
Qy 1164 GGGCTTCCCAAGAGAGGAGAAAGCTCTTCCCACTTTAAGACCTTGAATCTTAC 1223
Dh 1238 GGGCTTCCCAAGAGAGGAGAAAGCTCTTCCCACTTTAAGACCTTGAATCTTAC 1297
Qy 1224 AAGCATCCCTGATGCTTTTGTGATGCTGATGATGATGATGATGATGATGATGATGATG 1283
Dh 1298 AAGCATCCCTGATGCTTTTGTGATGCTGATGATGATGATGATGATGATGATGATG 1357
Qy 1284 TGCAGCGTGACTGTTGTGCTGAGAGCTTCAAGATATGATTAAGAGCTCTTGATGT 1343
Dh 1358 TGCAGCGTGACTGTTGTGCTGAGAGCTTCAAGATATGATTAAGAGCTCTTGATGT 1417
Qy 1344 CAATTCATATATGATCATGCAACAAGAGCCCTTAAGAGCTGAACAACAAGTCTGAG 1403
Dh 1418 CAATTCATATATGATCATGCAACAAGAGCCCTTAAGAGCTGAACAACAAGTCTGAG 1477
Qy 1404 TTGATATCTCGAAGACCGGCCCCCAAGAGCTCTGTATTTCCACAGCCATGAAATCATCC 1463
Dh 1478 TTGATATCTCGAAGACCGGCCCCCAAGAGCTCTGTATTTCCACAGCCATGAAATCATCC 1537
Qy 1464 AGGAGAGGCTGAGCGGGGTGTACCATGAGATGATGACCATATGGGTGGCATCCCTG 1523
Dh 1538 AGGAGAGGCTGAGCGGGGTGTACCATGAGATGATGACCATATGGGTGGCATCCCTG 1597
Qy 1524 CCGGAAATGATTAAGGGGAAAGGCTTCTGCTTATATTTGATGATGATGATGATGATGAT 1583
Dh 1598 CCGGAAATGATTAAGGGGAAAGGCTTCTGCTTATATTTGATGATGATGATGATGATGAT 1657

Qy 1584 CTTACAGTTTGTAAAGATTTGAGACATCTTGGAAAGCCCTGTATCATGACGAGACA 1643
Dh 1658 CTTACAGTTTGTAAAGATTTGAGACATCTTGGAAAGCCCTGTATCATGACGAGACA 1717
Qy 1644 CTGTCTCATGTCATCGCCAGGCTTTCTACGCTGAACGCTTCCAGCGCTTATGTGCAAC 1703
Dh 1718 CTGTCTCATGTCATCGCCAGGCTTTCTACGCTGAACGCTTCCAGCGCTTATGTGCAAC 1777
Qy 1704 CAGTATTTAAGAAATTTCCCTGAAAGCTTCTCTTCAAAAAGTTTCGGCTGGCTCAT 1763
Dh 1778 CAGTATTTAAGAAATTTCCCTGAAAGCTTCTCTTCAAAAAGTTTCGGCTGGCTCAT 1837
Qy 1764 CTTTCTCTCGGAGAGAGGCTCCAGTGGCAACTCTGATTAATTACAGCCATCGGCT 1823
Dh 1838 CTTTCTCTCGGAGAGAGGCTCCAGTGGCAACTCTGATTAATTACAGCCATCGGCT 1897
Qy 1824 CTGGGGAACAACAAGGCAACAAGTGAACAACAAGGAGAGAGGAGGAGGCTTCACTTG 1883
Dh 1898 CTGGGGAACAACAAGGCAACAAGTGAACAACAAGGAGAGAGGAGGCTTCACTTG 1957
Qy 1884 GTGCTCTGATGTTTATCTGACATCTCACTTTGAGAGAAATCAGTGAGGCTGCTCA 1943
Dh 1958 GTGCTCTGATGTTTATCTGACATCTCACTTTGAGAGAAATCAGTGAGGCTGCTCA 2017
Qy 1944 TTCTGACCCCAAGTTCTCACTGATTTGAGAGACTTTGCAAAATGCTAACAGTA 2003
Dh 2018 TTCTGACCCCAAGTTCTCACTGATTTGAGAGACTTTGCAAAATGCTAACAGTA 2077
Qy 2004 CAACCTTGAAAGAACTTGAAGTTGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 2063
Dh 2078 CAACCTTGAAAGAACTTGAAGTTGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 2137
Qy 2064 GAAAGCTGGAACAAGATTTGCAATCTGTGATTTCCAAAGATGCAAGCTTGGCCGAG 2123
Dh 2138 GAAAGCTGGAACAAGATTTGCAATCTGTGATTTCCAAAGATGCAAGCTTGGCCGAG 2197
Qy 2124 CAATGCTGAATTTTCTTACTTGTGATCAAAAAGAGTGAATGAATGAGGAGGAG 2183
Dh 2198 CAATGCTGAATTTTCTTACTTGTGATCAAAAAGAGTGAATGAATGAGGAGGAG 2257
Qy 2184 CTGCTCTCATCTTCTTCTGAAAGAAACCTTCTGCTTCTCTTCTCTCATGAATGG 2243
Dh 2258 CTGCTCTCATCTTCTTCTGAAAGAAACCTTCTGCTTCTCTTCTCTCATGAATGG 2317
Qy 2244 GCTTATGCTCTGAGAGATTTGAGAGCCGAGCATCTCCCTCATCTCAAGATTTGGTGT 2303
Dh 2318 GCTTATGCTCTGAGAGATTTGAGAGCCGAGCATCTCCCTCATCTCAAGATTTGGTGT 2377
Qy 2304 ACGGATTTTCAACTGGGCAACCTTGGCTCTCACTATTTGAATTTTTCAGACCCCAT 2363
Dh 2378 ACGGATTTTCAACTGGGCAACCTTGGCTCTCACTATTTGAATTTTTCAGACCCCAT 2437
Qy 2364 CTTGATGCTGGAATTTGGGATTTGCTGACTTGGCAGCTTCTTCTTCTCTCTTCTTGA 2423
Dh 2438 CTTGATGCTGGAATTTGGGATTTGCTGACTTGGCAGCTTCTTCTTCTCTCTTCTTGA 2497
Qy 2424 GGAACCGGACTCTTAATTTCTCTAGACAGACTGAGCTGAGCACTTATCTTACTTACT 2483
Dh 2498 GGAACCGGACTCTTAATTTCTCTAGACAGACTGAGCTGAGCACTTATCTTACTTACT 2557
Qy 2484 CTTTCTCTGAGCTCTGAGAAATTTCTCTGATATCTCTGTAATTTTGGGGGATA 2543
Dh 2558 CTTTCTCTGAGCTCTGAGAAATTTCTCTGATATCTCTGTAATTTTGGGGGATA 2617
Qy 2544 AGGGTGTTAACAACCTCCAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2602
Dh 2618 AGGGTGTTAACAACCTCCAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2677
Qy 2603 GCAACAGCACAACAATTTCAAGCAATTTTCAAGTCAAGTCTCCAGAAAGTGTGCAAGAT 2662
Dh 2678 GCAACAGCACAACAATTTCAAGCAATTTTCAAGTCAAGTCTCCAGAAAGTGTGCAAGAT 2737

Qy	2663	GCCATTTCGTAGAGTTTCCCTCAGAAAGGCCATGCTTTATATAAAGAAGAGTGTATT	2722
Db	2738	GCTATTTCGTAGAGTTTCCCTCAGAAAGGCCATGCTTTATATAAAGAAGAGTGTATT	2797
Qy	2723	GCTCTGCCAAGAGAGTCCCTTTTAAACCTCCCTCTTGATGAATTTCTTAAGGCTG	2782
Db	2798	GCTCTGCCAAGAGAGTCCCTTTTAAACCTCCCTCTTGATGAATTTCTTAAGGCTG	2857
Qy	2783	AAGGAATGAAGAAGATGGGGAATGGGGTATCTTTATCCCTTTTGTAATAACAGAGAGCA	2842
Db	2858	AAGGAATGAAGAAGATGGGGAATGGGGTATCTTTATCCCTTTTGTAATAACAGAGAGCA	2917
Qy	2843	GCCATGGGCTGGAGATCATATAGCCCTTCTTAGGCAAGATCTGTTCATCTGCCAGGCTATA	2902
Db	2918	GCCATGGGCTGGAGATCATATAGCCCTTCTTAGGCAAGATCTGTTCATCTGCCAGGCTATA	2977

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RESULT 10
US-09-724-676A-21453
; Sequence 21453, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OR INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21453
; LENGTH: 3622
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-21453

Query Match      82.9%   Score 3079;   DB 6;   Length 3622;
Best Local Similarity 91.6%   Pred. No. 0;
Matches 3435;   Conservative 0;   Mismatches 0;   Indels 316;   Gaps 4.

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Qy 744 TGACCCCTGCTCATCATCAATGACTTTGTTTCAGACCTATGACCTGTGCTTCC 803
Db 818 TGACCCCTGCTCATCATCAATGACTTTGTTTCAGACCTATGACCTGTGCTTCC 877
Qy 804 GCTACTTCCGGAGCTATTTGGTATCCGGCCGATGATTTACTTGTATTCCTCTGACGTG 863
Db 878 GCTACTTCCGGAGCTATTTGGTATCCGGCCGATGATTTACTTGTATTCCTCTGACGTG 937
Qy 864 AGCGCTGATTTGAACCTGTAGCTCTGAGAGTAGTGTTCCCTATTTATGTGTGACAGC 923
Db 938 AGCGCTGATTTGAACCTGTAGCTCTGAGAGTAGTGTTCCCTATTTATGTGTGACAGC 997
Qy 924 AGCATGATCTATTAATTAAGACATGCTCAATTAAGAGCGGAAATTTGTGAGAGCTGC 983
Db 998 AGCATGATCTATTAATTAAGACATGCTCAATTAAGAGCGGAAATTTGTGAGAGCTGC 1057
Qy 984 TTCCAGATCTACATGAACTCAACCAAGAACCTGTGACTTTGCTGCTTAATTTCTATG 1043
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Qy 1044 GACTGTACTGTGTGACGAGGCTGAGCAAGAACTTCGATGTGTGTGATGAACATCTTT 1103
Db 1118 GACTGTACTGTGTGACGAGGCTGAGCAAGAACTTCGATGTGTGTGATGAACATCTTT 1177
Qy 1104 TACCAAGATCGGTAAATAATGATATCAATATGACCTCAAGAGCTCAACCTTCAAGAGCGC 1163
Db 1178 TACCAAGATCGGTAAATAATGATATCAATATGACCTCAAGAGCTCAACCTTCAAGAGCGC 1237
Qy 1164 GGGCTTCCCAAGAAAGGAGAGAAAGCTCTTCCCACTTTAAGACCTTGAACCTTCTTAC 1223
Db 1238 GGGCTTCCCAAGAAAGGAGAGAAAGCTCTTCCCACTTTAAGACCTTGAACCTTCTTAC 1297
Qy 1224 AAGCATCCCTGATGATGCTTTTGTGATGCTGATGATGACAGGCTCTGTGATGAGACC 1283
Db 1298 AAGCATCCCTGATGATGCTTTTGTGATGCTGATGATGACAGGCTCTGTGATGAGACC 1357
Qy 1284 TGACGCGTGACTGTTGTGTGCTGACAGCTTCAAGATATGATTAACAGCTCTGTATGT 1343
Db 1358 TGACGCGTGACTGTTGTGTGCTGACAGCTTCAAGATATGATTAACAGCTCTGTATGT 1417
Qy 1344 CAATTCATATATATGATGATGACCAAGAGAGCTTAAAGAGTGAACACAGTACTAG 1403
Db 1418 CAATTCATATATATGATGATGACCAAGAGAGCTTAAAGAGTGAACACAGTACTAG 1477
Qy 1404 TTGATATCTGAGAAAGCCGGCCCGCCAAAGGCTGTATTTTCAACAGCCATGAAATCAATCC 1463
Db 1478 TTGATATCTGAGAAAGCCGGCCCGCCAAAGGCTGTATTTTCAACAGCCATGAAATCAATCC 1537
Qy 1464 AGGAGAGGCTGACGAGGAGTGTACATGAGACTGATGACCAATAGGAGTGCATCCCTG 1523
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Qy 1524 CCCGGAATATGTAAGGGGAAAGGCTTGTGCTTATATTTGGCATCTTGAACATTTCAAGT 1583
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Qy 1584 CTTACAGGTTTGTAAAGATTTGAGACCTCTTGAAGCCCTGTATCATGACGAGACA 1643
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Db 1718 CTGTCTCAGTGCATGCGCAGGCTTCTAGCTGAGAGGTTCCAGGCTTCAATGTGACACA 1777
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Db 1898 CTGGGAAACAGAGGCAAGTGAACAAAGGAGAGAGGAGGAGGCTTCACTTGG 1957
Qy 1884 GTGCTCTGATGTTTATCTACAGACTCCACTTTGAGAGAAATAGATGAGGCTGCTTA 1943
Db 1958 GTGCTCTGATGTTTATCTACAGACTCCACTTTGAGAGAAATAGATGAGGCTGCTTA 2017
Qy 1944 TTCCGACCCCAAGTTTCTACCTGATGTGAGAGACTTTGCAATGCTAATCAAGTA 2003
Db 2018 TTCCGACCCCAAGTTTCTACCTGATGTGAGAGACTTTGCAATGCTAATCAAGTA 2077
Qy 2004 CAACCTTGAAAGCTTGAAGTTGACAGAGTCAAGATTCACCCATTAAGCGCAAGGCTCA 2063
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Qy 2064 GAAAGCTGGAACAGATTTCTGCACTCTGTATGCCAAGATGTCAAGCTTGTGCGGAG 2123
Db 2138 GAAAGCTGGAACAGATTTCTGCACTCTGTATGCCAAGATGTCAAGCTTGTGCGGAG 2197
Qy 2124 CAATGCTGAATTTTCTTCTACTGTGTGATCAAAAAGAGGTATGAAATGAGGAGAG 2183
Db 2198 CAATGCTGAATTTTCTTCTACTGTGTGATCAAAAAGAGGTATGAAATGAGGAGAG 2257
Qy 2184 CTGCTCTCCATCTTCTCTGAAAGAACTTCTCTCTCTCTCTCTCTCATGAAATGG 2243
Db 2258 CTGCTCTCCATCTTCTCTGAAAGAACTTCTCTCTCTCTCTCTCTCATGAAATGG 2317
Qy 2244 GCTTATGCTCAGAGAGTGAAGAGCCGACATCCCTCTCACTCCAGAGTGGTGTGT 2303
Db 2318 GCTTATGCTCAGAGAGTGAAGAGCCGACATCCCTCTCACTCCAGAGTGGTGTGT 2377
Qy 2304 AAGGATTTTCACTGGGCAACCTTGTGCTCACTATGAAATTTTTCAGACCCCAT 2363
Db 2378 AAGGATTTTCACTGGGCAACCTTGTGCTCACTATGAAATTTTTCAGACCCCAT 2437
Qy 2364 CTTGATGCTGAAATGAGATGCTGAGACTTGTGAGCTTCTTCTCTCTCTCTTGTGACTA 2423
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Db 2618 AAGGATTTTAAACACCTCCAGCTTCTTCTC-TTTTTTTTTCTGAAAAAGAAAA 2677
Qy 2603 GCACACAGCACAAATTTCAAGCCATTTTCAGATCAAGATCCAGAAAGTGTGACAGAT 2662
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Qy 2663 GCGTATTCGTAGATTCCTCTGAGAAAGCCATGAGTTTAAAGAGAGTGTGAT 2722
Db 2738 GCGTATTCGTAGATTCCTCTGAGAAAGCCATGAGTTTAAAGAGAGTGTGAT 2797
Qy 2723 GCTGTGACAGAGAGCTCTCTTAAACTCTCTCTCTGATGAATTTCTTAAGGCTG 2782
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Qy 2843 GCCATGGCTGGAGATCATAGCCCTTCTAAGAGAAATCTGTGCTGCAAGGCTATA 2902
Db 2918 GCCATGGCTGGAGATCATAGCCCTTCTAAGAGAAATCTGTGCTGCAAGGCTATA 2977
Qy 2903 GTAAATTAATTAATTTGCAATTTGAATATAATCTGTGTTTCTTAAATGGAAGAC 2962

Db 2978 GTAAATTACTATTTTGCATTTGAAATATATCTGCTGTTTCTTAAATGTGAAGAC 3037
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 Qy 3023 CCAACAGTGTCTCTCTGTTTGTGAGCTAAGTAAAGAGAGACATCTCTGTCTTTAA 3082
 Db 3098 CCAACAGTGTCTCTCTGTTTGTGAGCTAAGTAAAGAGAGACATCTCTGTCTTTAA 3157
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 Qy 3203 GGAAGTTGAAATGGGGGCTACATATGCCCTCTCTCCCTCTACAAAGATGTGTTT 3262
 Db 3184 ----- 3183
 Qy 3263 TCCATCTGATCTCTGCACTCTGTGAGGGAGAAAGGGGCGCTGGTATCTAGAGATT 3322
 Db 3184 ----- 3183
 Qy 3323 GTTGAATTCCTGTCTATCCCTCTCTATCCACCCCTGCTGATATATGTAGCCCAT 3382
 Db 3184 ----- 3183
 Qy 3383 ACCCCAAATTAATCTATATTAAGACACCCCGACAGTTTCTGCTGCTCTTTGCT 3442
 Db 3184 ----- 3442
 Qy 3443 GCCATGTTTTCACAGAGAGAAAGATCTGCTATTTTTCATATTTTACTATT 3502
 Db 3240 GCCATGTTTTCACAGAGAGAAAGATCTGCTATTTTTCATATTTTACTATT 3299
 Qy 3503 ATGATGATTTTAAAGTGTATTTTAAAGACAGATCTGTTAGGGGTGGAGGAGATATT 3562
 Db 3300 ATGATGATTTTAAAGTGTATTTTAAAGACAGATCTGTTAGGGGTGGAGGAGATATT 3359
 Qy 3563 GAGGGAGGCTGGGCTCTTGGGAAAGAAATGGGGAAGCAATTTTATTTAAAGTTACT 3622
 Db 3360 GAGGGAGGCTGGGCTCTTGGGAAAGAAATGGGGAAGCAATTTTATTTAAAGTTACT 3419
 Qy 3623 ATTGCTCTACTTGTATTTTTCAGAAATGGCAATATCAATATTAAGTATATGAT 3682
 Db 3420 ATTGCTCTACTTGTATTTTTCAGAAATGGCAATATCAATATTAAGTATATGAT 3479
 Qy 3683 TTTAATGTAATAAATTTTATGATTTTAA 3713
 Db 3480 TTTAATGTAATAAATTTTATGATTTTAA 3510

RESULT 11
 US-09-724-676-21451
 ; Sequence 21451, Application US/09724676
 ; GENERAL INFORMATION:
 ; APPLICANT: Compugen LTD
 ; TITLE OF INVENTION: Variants of alternative splicing
 ; FILE REFERENCE: 129181.4 Compugen
 ; CURRENT APPLICATION NUMBER: US/09/724,676
 ; NUMBER OF SEQ ID NOS: 97222
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 21451:
 ; LENGTH: 3439
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-724-676-21451

Query Match 76.0%; Score 2821; DB 6; Length 3439;

Best Local Similarity 88.5%; Pred. No. 0;
 Matches 3288; Conservative 0; Mismatches 0; Indels 427; Gaps 4;

Qy 1 ATTAACAGCCGCTGTAGAGAGACGAGAGAGGCGCTTCCCTCTTTGGACCTTTTGA 60
 Db 38 ATTAACAGCCGCTGTAGAGAGACGAGAGAGGCGCTTCCCTCTTTGGACCTTTTGA 97
 Qy 61 TGCCTGTTTTTTTTTCAATGTGCTTGTCTGGAGCGCAAGTCCACAGACAGCTTA 120
 Db 98 TGCCTGTTTTTTTTTCAATGTGCTTGTCTGGAGCGCAAGTCCACAGACAGCTTA 157
 Qy 121 AGCTTACTTTCTGTGAAAGGAGAAAGTATCCCTGTGAAAGCGTTTAACTTTGAG 180
 Db 158 AGCTTACTTTCTGTGAAAGGAGAAAGTATCCCTGTGAAAGCGTTTAACTTTGAG 217
 Qy 181 GGGGTGCGGACGTGAGTTTCTCCCATGCCAGCGCAATGTGTGCTTGGACCTGTC 240
 Db 218 GGGGTGCGGACGTGAGTTTCTCCCATGCCAGCGCAATGTGTGCTTGGACCTGTC 277
 Qy 241 AGAGCCGCGCTCGACGTGCTGAGGGAGG-CCCGAGAGGGGCGGGAGTGGCCACAGA 299
 Db 278 AGAGCCGCGCTCGACGTGCTGAGGGAGG-CCCGAGAGGGGCGGGAGTGGCCACAGA 337
 Qy 300 ACGCGGTTCTGTAAAGACGTTGGAGATTCGATTCGAGAAAGAGAAACCGGAT 359
 Db 338 ACGCGGTTCTGTAAAGACGTTGGAGATTCGATTCGAGAAAGAGAAACCGGAT 397
 Qy 360 TGAAGAGAGCAGAGCCGCTGAGGGGAGGGGCTGTAGATGTGCTGCGCTCCCG 419
 Db 398 TGAAGAGAGCAGAGCCGCTGAGGGGAGGGGCTGTAGATGTGCTGCGCTCCCG 457
 Qy 420 GGGCGTGTCTGAGTGGTGGTTTTTTCATCTTGTATCCCGGCTCTCTCTGATCTTGT 479
 Db 458 GGGCGTGTCTGAGTGGTGGTTTTTTCATCTTGTATCCCGGCTCTCTCTGATCTTGT 517
 Qy 480 CCTGAGCATCTGAATCAAGAGACCCATGCGATCTGAGTGCCTTATGCTCTGGCATGC 539
 Db 518 CCTGAGCATCTGAATCAAGAGACCCATGCGATCTGAGTGCCTTATGCTCTGGCATGC 577
 Qy 540 CCATCAAGAAATAGCGCATGAGGTGTGATCTCTAGAGAGAGCAACATATTAAGA 599
 Db 578 CCATCAAGAAATAGCGCATGAGGTGTGATCTCTAGAGAGAGCAACATATTAAGA 637
 Qy 600 CAACCTCATGAGCTTGTAAAGGTGCATCCAGTTAGGATTAACCACTGTGGGAGCC 659
 Db 638 CAACCTCATGAGCTTGTAAAGGTGCATCCAGTTAGGATTAACCACTGTGGGAGCC 697
 Qy 660 TGAATCAAAACAGAGCGTATGCTCTCATGCAAGATTTCTTACGTGTGAGAGTACT 719
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 Db 758 TCTTCCAGTGAAGGAGAGCACTGACCCCTGCTCATCAATCAATGACTTTGTTTCA 817
 Qy 780 AGACCTATGACCTGTGCTCTTCCGCTACTTCCGGAGCTAATTTGTATCCGGCCGATG 839
 Db 818 AGACCTATGACCTGTGCTCTTCCGCTACTTCCGGAGCTAATTTGTATCCGGCCGATG 877
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 Db 938 GTTCCCTATTCATGATGTGTCAGAGAGATGATCATTAATTAAGACAGTCAACATAAG 997
 Qy 960 AGGCGGAATTTCTGAGAGAGTGTCTTCAGAGATCAATCAAGAACTCAACGAACCTTC 1019
 Db 998 AGGCGGAATTTCTGAGAGAGTGTCTTCAGAGATCAATCAAGAACTCAACGAACCTTC 1057
 Qy 1020 GGAATTTGCTGCTTAATTTCTATGATGTGATCTGTGTCAGAGAGTGGCAAGAACTTC 1079

Dh 1058 GGACTTGTCTGCTAAATCTATGACTGTACTGTGTGACGAGCAGATGCGAAGACATTC 1117
Qy 1080 GGATTGTGTGATGAAACAATCTTTTACCAAGATGGTAAATATGATATCAATATGAC 1129
Dh 1118 GGATTGTGTGATGAAACAATCTTTTACCAAGATGGTAAATATGATATCAATATGAC 1177
Qy 1140 TCAAGGCTCAACCTTCAACAACGGGCGGCTTCCAGAAAAGCAGAGAGCTCTTCCCA 1199
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Qy 1200 CATTTAAAGACTTGAATCTTTTCAAGACATCCCTGATGCTTTTGTGATGTGACA 1259
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Qy 1260 TGTACAACGCTCTCTGTAAAGACCTGACGCTGACTGTTGTGTGTGAGAGCTTCAAGA 1319
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Dh 1358 TAATGATTAAGGCTCTTGTATGTCAATCCATTAATATGATATGACACAGAGAGCTT 1417
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Qy 1440 ATTCCACAGGCTTGAATCCATTCAGAGGAGGCTCGACGGGCTGTCAATGAGACTG 1499
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Qy 1500 ATGACATATGCTGTGACATCCCTGCGGGAATGTAAGAGGGAAGGCTTGTGCTTTATA 1559
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Qy 1560 TTGCAATCATTTGACATTTCAAGTCTTAAGAGGTTGTTAAAGTTGAGACATCTTGA 1619
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Qy 1680 GGTTCAGACGCTTCAATGTGCAACAAGATTTTAAAGAGATTCCTTGAAGCTTCTCTT 1739
Dh 1718 GGTTCAGACGCTTCAATGTGCAACAAGATTTTAAAGAGATTCCTTGAAGCTTCTCTT 1762
Qy 1740 CCAAAAAGTTTGGCTGTGCTCAATCTTTCTCTGCGCAGACAGGCTCCAGTGCACATCTCT 1799
Dh 1763 ----- 1762
Qy 1800 GCATTACTTACAGCAGCATGCGTCTGTGGGGAACAACAAGCACAAGTGCACAAAGGCGAG 1859
Dh 1763 ----- 1762
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Dh 1763 -----GGTTCACCTTGTGCTCTGATGTTTTCACCTGACACTCCACTTGG 1810
Qy 1920 AGGAATCATGAGGAGCTGCGCTTATTCCTGACCCCAAGTTTCTCACTTGAAGTGAAGA 1979
Dh 1811 AGGAATCATGAGGAGCTGCGCTTATTCCTGACCCCAAGTTTCTCACTTGAAGTGAAGA 1870
Qy 1980 CTTTGAAGTCTTAACTTCAAGTACAACTTGAAGAGCTTGAAGTTGCAAGTCAAGGT 2039
Dh 1871 CTTTGAAGTCTTAACTTCAAGTACAACTTGAAGAGCTTGAAGTTGCAAGTCAAGGT 1930
Qy 2040 TCACCCATTAAGGCGCAAGGCTTCAAGAGACCTGGAACAAGATTCGACATCTGTGATC 2099
Dh 1931 TCACCCATTAAGGCGCAAGGCTTCAAGAGACCTGGAACAAGATTCGACATCTGTGATC 1990
Qy 2100 CCAAGATGTACGCTTGTGCGCAGAGATGTGAATTTTCTTCACTTGTGATCAAAAAA 2159
Dh 1991 CCAAGATGTACGCTTGTGCGCAGAGATGTGAATTTTCTTCACTTGTGATCAAAAAA 2050

Qy 2160 GGAGGTATATGAAGTGAAGGAGAGCTGCTCTCCATCTTCTTCTGGAAGAACTTCT 2219
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Qy 2220 CTCCTTCTCTTCTCAATGAATGGGCTTGAAGCTTCAAGAGAGTGAAGACCGAGATC 2279
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Dh 2531 GAACTCCAGAGTGTGAACAAGATGCTTATTCGTAGAGTTCCTCAAGAGGCAATGCTG 2590
Qy 2699 TTTTGAAGAGAAAGTGAAGTGTGCTCTGACAGACAGCTCTCTTAACTCTCTCT 2758
Dh 2591 TTTTGAAGAGAAAGTGAAGTGTGCTCTGACAGACAGCTCTCTTAACTCTCTCTCT 2650
Qy 2759 CTCTGATGATTTCTTAAAGCTGTAAGAAATGAAGAGTGGGATTAATCTTTTA 2818
Dh 2651 CTCTGATGATTTCTTAAAGCTGTAAGAAATGAAGAGTGGGATTAATCTTTTA 2710
Qy 2819 TCCCTTTTGTAAACAGAGGAGCCATGGGCTGGAGATCATAGCCCTTCTAGGAG 2878
Dh 2711 TCCCTTTTGTAAACAGAGGAGCCATGGGCTGGAGATCATAGCCCTTCTAGGAG 2770
Qy 2879 AATCCTGTACCTGCGCAGGCTATGTAATTAATTAATTTTGAATTTGAATATATCT 2938
Dh 2771 AATCCTGTACCTGCGCAGGCTATGTAATTAATTAATTTTGAATTTGAATATATCT 2830
Qy 2939 GGTGTTTTCCTAATGTGAAGACTTACCAATGAATTTTGAATCTTCTCCAGAGAGA 2998
Dh 2831 GGTGTTTTCCTAATGTGAAGACTTACCAATGAATTTTGAATCTTCTCCAGAGAGA 2890
Qy 2999 TTTTTCCTTCTCTCATCTTTTCAACAGTGTCTCTGTGTTGAGAGTAAAGTAA 3058
Dh 2891 TTTTTCCTTCTCTCATCTTTTCAACAGTGTCTCTGTGTTGAGAGTAAAGTAA 2950
Qy 3059 GAGGGGACATCTTGTCTGTTTAAACAAGTGCATATCTGTGAGGCGCAGAAATATTTT 3118
Dh 2951 GAGGGGACATCTTGTCTGTTTAAACAAGTGCATATCTGTGAGGCGCAG----- 3000
Qy 3119 CTTAAACTCATGGGGAACAAGATTTCTGCTTGTGAGGTCAATGCTGTGCATATG 3178
Dh 3001 ----- 3000
Qy 3179 TCCTAACCCCTGTCTTCATGACGAGAAATTGAATGGGGCTTACATATGCTCTCTCT 3228
Dh 3001 ----- 3000

QY 3239 CCCCCTCACAAGAGTTGTGTGTTTCCATCTGATCCCTTCACTCTTGTCAAGGGAGAAG 3238
Db 3001 ----- 3000
QY 3299 GGGGCTGTATCTCAGCAGATTTGTAATTCCTTCTTCAATCCCTTCTTCAATCC 3358
Db 3001 ----- 3000
QY 3359 TGCCTGTAATATGTATGACCCCAATACCCCAATATATCTCTATATTAACACCCCA 3418
Db 3001 ----- CAATATACCTCTATATATTAACACCCCAATCC 3032
QY 3419 AGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3478
Db 3033 AGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3092
QY 3479 TTTTCTTCTTCAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3538
Db 3093 TTTTCTTCTTCAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3152
QY 3539 TGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3598
Db 3153 TGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3212
QY 3599 GCAACATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3658
Db 3213 GCAACATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3272
QY 3659 TACAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3713
Db 3273 TACAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3327

RESULT 12
US-09-724-676A-21451
; Sequence 21451, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; NUMBER OF SEQ ID NOS: 2000-11-28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 21451
; LENGTH: 3439
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-21451

Query Match 76.0%; Score 2821; DB 6; Length 3439;
Best Local Similarity 88.5%; Pred. No. 0;
Matches 3288; Conservative 0; Mismatches 0; Indels 427; Gaps 4;
QY 1 ATTAACAGGCGCGTGTAG 60
Db 38 ATTAAAGGCGCGTGTAG 97
QY 61 TGCCTGCTTCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 98 TGCCTGCTTCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 157
QY 121 AGCTTCTCTCTGTAAG 180
Db 158 AGCTTCTCTCTGTAAG 217
QY 181 GGGGTGCGGAGCGTGAATTTCTCCATGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Db 218 GGGGTGCGGAGCGTGAATTTCTCCATGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 277
QY 241 AGGAGCGCGCTGCACTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 299
Db 278 AGGAGCGCGCTGCACTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 337

QY 300 AGCGGGTCTGTAAAG 359
Db 338 AGCGGGTCTGTAAAG 397
QY 360 TGAAG 419
Db 398 TGAAG 457
QY 420 GGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 479
Db 458 GGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 517
QY 480 CTTGAGATCTGAGATCAAG 539
Db 518 CTTGAGATCTGAGATCAAG 577
QY 540 CCATCAAG 599
Db 578 CCATCAAG 637
QY 600 CAACCTCATGAGCTTGAAG 659
Db 638 CAACCTCATGAGCTTGAAG 697
QY 660 TGAATACCAAG 719
Db 698 TGAATACCAAG 757
QY 720 TCTTCCAGTGAAG 779
Db 758 TCTTCCAGTGAAG 817
QY 780 AGACCTATGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 839
Db 818 AGACCTATGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 877
QY 840 ATTACTGTATTTCCCTGTCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 899
Db 878 ATTACTGTATTTCCCTGTCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 937
QY 900 GTTCCCTATTTATGATGCTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 959
Db 938 GTTCCCTATTTATGATGCTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 997
QY 960 AGGCGGAATTTCTGAG 1019
Db 998 AGGCGGAATTTCTGAG 1057
QY 1020 GGAATTTGCTGCTTAATTTCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1079
Db 1058 GGAATTTGCTGCTTAATTTCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1117
QY 1080 GGAATTTGCTGATGAACAATTTCTTACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1139
Db 1118 GGAATTTGCTGATGAACAATTTCTTACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1177
QY 1140 TCAAGAGCTCAACCTAACAAG 1199
Db 1178 TCAAGAGCTCAACCTAACAAG 1237
QY 1200 CATTTAAAG 1259
Db 1238 CATTTAAAG 1297
QY 1260 TGTAAAGAGCTCTGTAAG 1319
Db 1298 TGTAAAGAGCTCTGTAAG 1357
QY 1320 TAATGATTAAG 1379
Db 1358 TAATGATTAAG 1417

QY 1380 TAAGAGTGAACAAGTACTGAGTGAATCTGAGAGACCGGCCCCCAAAAGGCTCTGT 1439
 DB 1418 TAACAGAGGAACAAGTACTGAGTGAATCTGAGAGACCGGCCCCCAAAAGGCTCTGT 1477
 QY 1440 ATTCCAGAGGCAATGGAATCCATCCAGGAGAGGCTCCGACGGGGTGTACATGAGACTG 1499
 DB 1478 ATTCCAGAGGCAATGGAATCCATCCAGGAGAGGCTCCGACGGGGTGTACATGAGACTG 1537
 QY 1500 ATGACATATGGGTGGCATGCTCCGCGGAAATGTAAGGGGAAAGGCTTGCTGCTTATA 1559
 DB 1538 ATGACATATGGGTGGCATGCTCCGCGGAAATGTAAGGGGAAAGGCTTGCTGCTTATA 1597
 QY 1560 TTGSCATCATGACATTTCTACAGTCTTACAGGTTGTTAAGAGTTGAGACACTTTGGA 1619
 DB 1598 TTGSCATCATGACATTTCTACAGTCTTACAGGTTGTTAAGAGTTGAGACACTTTGGA 1657
 QY 1620 AAGCCCTGTGATCATGACGGAACACTGTCTCATGTGATGCGCCAGGCTTCTACGCTGAC 1679
 DB 1658 AAGCCCTGTGATCATGACGGAACACTGTCTCATGTGATGCGCCAGGCTTCTACGCTGAC 1717
 QY 1680 GGTTCAGACGCTTGATGTCAGAACACAGATTTTAAGAGATTCCTTGAAAGCTTCTCTT 1739
 DB 1718 GGTTCAGACGCTTGATGTCAGAACACAGATTTTAAGAGATTTCTCT----- 1762
 QY 1740 CCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCAGTGCAACTCT 1799
 DB 1763 ----- 1762
 QY 1800 GCATTACTTACCAAGCATGGTCTCTGGGGAAACACAGGCAACAGTGAACAAAGGCGAG 1859
 DB 1763 ----- 1762
 QY 1860 AAGTGAAGCCAGGCGTTCACTTGTTGTCCTGATGTTTTCCTCAGACTCCACTTTGG 1919
 DB 1763 -----GGTTTCACTTGTTGTCCTGATGTTTTCCTCAGACTCCACTTTGG 1810
 QY 1920 AGGAATCAGTGAAGGCTCGCTCATTTCTGACCCCAAGTTTCTCACTCTAGTTGAGAGA 1979
 DB 1811 AGGAATCAGTGAAGGCTCGCTCATTTCTGACCCCAAGTTTCTCACTCTAGTTGAGAGA 1870
 QY 1980 CTTTGCAATGCTTAATCAAGTACAACTTTGAAAAGCTTGAAGTTGACAGTCAAGT 2039
 DB 1871 CTTTGCAATGCTTAATCAAGTACAACTTTGAAAAGCTTGAAGTTGACAGTCAAGT 1930
 QY 2040 TCACCAATTAGCCGCAAGGCTCAGAGACCTGAGAACAGATTCGATCTCTGTATC 2099
 DB 1931 TCACCAATTAGCCGCAAGGCTCAGAGACCTGAGAACAGATTCGATCTCTGTATC 1990
 QY 2100 CCAAGATGTCAGGCTTGCCCGCAGCAATGTGAATTTTCTTCTACTTGATGATCAAAAA 2159
 DB 1991 CCAAGATGTCAGGCTTGCCCGCAGCAATGTGAATTTTCTTCTACTTGATGATCAAAAA 2050
 QY 2160 GAGTGTATATGAAGTGAAGGAGCTGCTCTCAATCTTCTCTGAGAAAGAACTTCT 2219
 DB 2051 GAGTGTATATGAAGTGAAGGAGCTGCTCTCAATCTTCTCTGAGAAAGAACTTCT 2110
 QY 2220 CT 2279
 DB 2111 CT 2170
 QY 2280 CCTCTCACTCAGAGTGGGTGTACGGAATTTCAATGCGCAACCTTTGCTCTCACTA 2339
 DB 2171 CCTCTCACTCAGAGTGGGTGTACGGAATTTCAATGCGCAACCTTTGCTCTCACTA 2230
 QY 2340 TTGAATTTTTCAGACCCCAATTTCTCATGCTGAGAAATGAGATTTGCTGACCTTGAGC 2399
 DB 2231 TTGAATTTTTCAGACCCCAATTTCTCATGCTGAGAAATGAGATTTGCTGAGCCTTGAGC 2290
 QY 2400 TTTCTTCCCTGCTGCTTGAAGTGAAGGAGCTGAGTCTTAATTTCTCTGAGACAGTATG 2459
 DB 2291 TTTCTTCCCTGCTGCTTGAAGTGAAGGAGCTGAGTCTTAATTTCTCTGAGACAGTATG 2350
 QY 2460 TGGAATATATCCCTAGTCTTCTCTCTGATCTCTGAGAAAGATATCTCTGTAT 2519

DB 2351 TGGAATATATCCCTAGTCTTCTCTCTGATCTCTGAGAAAGATATCTCTGTAT 2410
 QY 2520 CTCTGTAAGGTTTGGGGGATTAAGGTGTTTAAACAACCTCCCAAGCTTCTCTTCTT 2578
 DB 2411 CTCTGTAAGGTTTGGGGGATTAAGGTGTTTAAACAACCTCCCAAGCTTCTCTTCTT 2470
 QY 2579 TTTTCTTCTGAAAAAAGAAAAAGCAACAGACACAAATTTCAAGCAATTTTCAGATCA 2638
 DB 2471 TTTTCTTCTGAAAAAAGAAAAAGCAACAGACACAAATTTCAAGCAATTTTCAGATCA 2530
 QY 2639 GAACTCAGAAATGTTGACAAAGATGCTTATCTGAGATTCCTCAGAGAGCCATGCTG 2698
 DB 2531 GAACTCAGAAATGTTGACAAAGATGCTTATCTGAGATTCCTCAGAGAGCCATGCTG 2590
 QY 2699 TTTATGAAGAGAAAGTATGATGCTCTGACAGACAGTCTCTTTAAATCTCTCT 2758
 DB 2591 TTTATGAAGAGAAAGTATGATGCTCTGACAGACAGTCTCTTTAAATCTCTCTCT 2650
 QY 2759 CTCTGATGAATTTCTTAAGGCTGAGGAATGAGAGAGTGGGACATGGGATATCTTTA 2818
 DB 2651 CTCTGATGAATTTCTTAAGGCTGAGGAATGAGAGAGTGGGACATGGGATATCTTTA 2710
 QY 2819 TCCCTTTTGTAAAAACAGAGGCAAGCCATGGGCTGGAGATCATAGCCCTTCTAGGAG 2878
 DB 2711 TCCCTTTTGTAAAAACAGAGGCAAGCCATGGGCTGGAGATCATAGCCCTTCTAGGAG 2770
 QY 2879 AATCTGTGACCTGCGCAGGCTATATGTAATTTATCTATTTTGCATTTGAAATATCT 2938
 DB 2771 AATCTGTGACCTGCGCAGGCTATATGTAATTTATCTATTTTGCATTTGAAATATCT 2830
 QY 2939 GGTGTTTCTTAATGTAAGAACCTTACCAATGAATTTTATGATCATTTCCAGAGAGA 2998
 DB 2831 GGTGTTTCTTAATGTAAGAACCTTACCAATGAATTTTATGATCATTTCCAGAGAGA 2890
 QY 2999 TTTTCTTGTCTCTCTCATCTTTTCAACAGTGTCTCTGTTTGTGAGCTAAGTAA 3058
 DB 2891 TTTTCTTGTCTCTCTCATCTTTTCAACAGTGTCTCTGTTTGTGAGCTAAGTAA 2950
 QY 3059 GAGGGACACTCTGTCTGTTTAAACAGACGCTCATATCTGTGAGGCAAGAAATATTT 3118
 DB 2951 GAGGGACACTCTGTCTGTTTAAACAGACGCTCATATCTGTGAGGCAAG----- 3000
 QY 3119 CTTAACTCATAGGGGAGAACAGACATTTCTTGCTGTGAGGTATTTGCTGTGCATATG 3178
 DB 3001 ----- 3000
 QY 3179 TCTAACCCTCTGCTTCATGACAGGAAGTTGAAATGGGGGCTACATATGCTCTCT 3238
 DB 3001 ----- 3000
 QY 3239 CCCCCTCATAGAGTGTGTGTTTTCATCTGATCTTCACTCTGTCAAGGGAGAGAG 3298
 DB 3001 ----- 3000
 QY 3299 GGGGCTGTATCTCAGGACATTTGTAATCTCTGTCTATCCCTTCTATCCACCC 3358
 DB 3001 ----- 3000
 QY 3359 TGCTGTATATATGTTAGCCATACCCCAATTAAGTCTATATTAAGACACCCCGAGC 3418
 DB 3001 -----CAATTAAGTCTATATTAAGACACCCCGAGC 3032
 QY 3419 AGTTTCTGCTGCTGCTGCTTCTGCTGCTGCTTCTTCAAGAGAGAAATTTCTTGCTA 3478
 DB 3033 AGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTTCTTCAAGAGAGAAATTTCTTGCTA 3092
 QY 3479 TTTTCTTCTAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3538
 DB 3093 TTTTCTTCTAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3152
 QY 3539 TGTTAGGGGTGGAGGAAATTTTGAAGGAGGCTGGGTCTTGAAGGAAAGAAATGGGAA 3598

CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 21454
LENGTH: 3475
TYPE: DNA
ORGANISM: Homo sapiens
US-09-724-676A-21454

Query Match 74.7%; Score 2775; DB 6; Length 3475;
Best Local Similarity 87.7%; Pred. No. 0;
Matches 3288; Conservative 0; Mismatches 0; Indels 463; Gaps 5;

QY 1 ATTTACAGGCGCTGTGTAAGAGACGAGAGAGGCGCTGCTCTTTGGGACCTTTCA 60
DB 38 ATTTACAGGCGCTGTGTAAGAGACGAGAGAGGCGCTGCTCTTTGGGACCTTTCA 97
QY 61 TGCCCTGTTTTTTTTCAGATGTGGCTTGCTGGGCGCAAGCTCCAGCAGCCAGCTTA 120
DB 98 TGCCCTGTTTTTTTTCAGATGTGGCTTGCTGGGCGCAAGCTCCAGCAGCCAGCTTA 157
QY 121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCTGTGAAAGCGGTTAAACTTTGAG 180
DB 158 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCTGTGAAAGCGGTTAAACTTTGAG 217
QY 181 GGGGTGCGGAGCGTGAATTTCTTCCCATGCGAGGAGATGTGTGGCTTTGAGCTGTCC 240
DB 218 GGGGTGCGGAGCGTGAATTTCTTCCCATGCGAGGAGATGTGTGGCTTTGAGCTGTCC 277
QY 241 AGGAGCGGCGTGAAGTGTCTGAGGAGAGG-CCCGAGGGGGGGGGAGGTTGAGCCACAGA 299
DB 278 AGGAGCGGCGTGAAGTGTCTGAGGAGAGG-CCCGAGGGGGGGGGAGGTTGAGCCACAGA 337
QY 300 AGCGGCGTCTGTAAAGAGACGTTGGAGATTCATTCGAGAAAGAGAGAACCGGAT 359
DB 338 AGCGGCGTCTGTAAAGAGACGTTGGAGATTCATTCGAGAAAGAGAGAACCGGAT 397
QY 360 TGAAGAGAGCGAGCGCTGAGGGGAGGGGCTGCTAAATGTGGCTTCTCTCG 419
DB 398 TGAAGAGAGCGAGCGCTGAGGGGAGGGGCTGCTAAATGTGGCTTCTCTCG 457
QY 420 GGGCGGCGTCTGAGGCTGTTTTTTCATCTTTGATCCGCGGCTCTCTGAGCTGTG 479
DB 458 GGGCGGCGTCTGAGGCTGTTTTTTCATCTTTGATCCGCGGCTCTCTGAGCTGTG 517
QY 480 CCTCAGCATCTGAATCAAGAGACCCATGCACTGA----- 516
DB 518 CCTCAGCATCTGAATCAAGAGACCCATGCACTGA----- 577
QY 517 -----GGTGCCTTATGCTCTTGCGCATGCGCCATCAAGAAATAGCCATAGAA 563
DB 578 CTTACATCTCATTGTGCTTATGCTCTTGCGCATGCGCCATCAAGAAATAGCCATAGAA 637
QY 564 GTGTGATCTCTCAGAGAGACACATATTAAGAAACAACCTCATCAGCTTTGAAAGT 623
DB 638 GTGTGATCTCTCAGAGAGACACATATTAAGAAACAACCTCATCAGCTTTGAAAGT 697
QY 624 CCATCCAGTTAGGATTAACCACTGTGGGAGGCTGAGTACCAACCAAGCGTATG 683
DB 698 CCATCCAGTTAGGATTAACCACTGTGGGAGGCTGAGTACCAACCAAGCGTATG 757
QY 684 TCTCATGCAAGATTTCTAGTGTGAGAGTATCTTTTCCCACTGAGAGGAGAAC 743
DB 758 TCTCATGCAAGATTTCTAGTGTGAGAGTATCTTTTCCCACTGAGAGGAGAAC 817
QY 744 TGAACCCCTGCTACCTCAATGACCTTTGTTCAAGACCTATGACCTGTGCTTCC 803
DB 818 TGAACCCCTGCTACCTCAATGACCTTTGTTCAAGACCTATGACCTGTGCTTCC 877
QY 804 GCTACTTCCGGAGCTATTTGATCCGGCCGAGATTAATTGATATCCCTCTGAGTG 863
DB 878 GCTACTTCCGGAGCTATTTGATCCGGCCGAGATTAATTGATATCCCTCTGAGTG 937

QY 864 AGCCGCTGATTTGAATCTGTAGCTCTGAGCTAGTGTGCTCCATTCTATGTGCCAGC 923
DB 938 AGCCGCTGATTTGAATCTGTAGCTCTGAGCTAGTGTGCTCCATTCTATGTGCCAGC 997
QY 924 ACATGAGTTCATTAATTAACAGTCCACATTAAGAGGCGGAAATTTCTCAGAGCTGC 983
DB 998 ACATGAGTTCATTAATTAACAGTCCACATTAAGAGGCGGAAATTTCTCAGAGCTGC 1057
QY 984 TTCAGATATCTACATGAACCTCAACCAAAACCTCGAGCTTGTGCTTAATTTATG 1043
DB 1058 TTCAGATATCTACATGAACCTCAACCAAAACCTCGAGCTTGTGCTTAATTTATG 1117
QY 1044 GACTGTACTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1103
DB 1118 GACTGTACTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1177
QY 1104 TACCAAGATCGGTAAATATGATATCAATATATGACCTCAAAAGGCTCAACCTACAAAGCGC 1163
DB 1178 TACCAAGATCGGTAAATATGATATCAATATATGACCTCAAAAGGCTCAACCTACAAAGCGC 1237
QY 1164 GGGCTTCCAGAAAGAGCGAGAGAGAGGCTTCCCATTTTAAAGACCTAGACTTTTAC 1223
DB 1238 GGGCTTCCAGAAAGAGCGAGAGAGGCTTCCCATTTTAAAGACCTAGACTTTTAC 1297
QY 1224 AAGACATCCCGATGATGCTTTTTTTTGGATGCTGACATGTACAAAGCTCTCTGTAAGACC 1283
DB 1298 AAGACATCCCGATGATGCTTTTTTTTGGATGCTGACATGTACAAAGCTCTCTGTAAGACC 1357
QY 1284 TGACGCTGACTGTTTGGTGTGCTGAGAGCTTCAAGATATATGATTAAGCTCTTGAATG 1343
DB 1358 TGACGCTGACTGTTTGGTGTGCTGAGAGCTTCAAGATATATGATTAAGCTCTTGAATG 1417
QY 1344 CAATCCATATATATGATATATGATATGATATGATATGATATGATATGATATGATATG 1403
DB 1418 CAATCCATATATATGATATATGATATGATATGATATGATATGATATGATATGATATG 1477
QY 1404 TTGATATCTGAGAGCGGCGCCCGCAAAAGGCTGTATTTCCAGAGCCATGATATCCATCC 1463
DB 1478 TTGATATCTGAGAGCGGCGCCCGCAAAAGGCTGTATTTCCAGAGCCATGATATCCATCC 1537
QY 1464 AGGAGAGGCTGAGCGGGGTGTATCAATGAGACTGATGACCATATGAGGTGATCCCTG 1523
DB 1538 AGGAGAGGCTGAGCGGGGTGTATCAATGAGACTGATGACCATATGAGGTGATCCCTG 1597
QY 1524 CCGGGAATATGTAAGGGGAAAGGCTTCTGCTTATATTTGGATATGATGATATGATGAT 1583
DB 1598 CCGGGAATATGTAAGGGGAAAGGCTTCTGCTTATATTTGGATATGATGATATGATGAT 1657
QY 1584 CTTACAGGTTTGTAAAGAGTTGAGACCTTTGAAAGGCTGTATGATGATGATGATGATG 1643
DB 1658 CTTACAGGTTTGTAAAGAGTTGAGACCTTTGAAAGGCTGTATGATGATGATGATGATG 1717
QY 1644 CTGTCTAGTGCATGCGCCAGGCTTCTAGCTGTAAGGCTTCAAGGCTTCAATGTGCAACA 1703
DB 1718 CTGTCTAGTGCATGCGCCAGGCTTCTAGCTGTAAGGCTTCAAGGCTTCAATGTGCAACA 1777
QY 1704 CAGTATTTAAAGATTTCCCTTGAAGCTTCTCTTCCAAAAAGTTTCGTGGCTCAT 1763
DB 1778 CAGTATTTAAAGATTTCCCTTGAAGCTTCTCTTCCAAAAAGTTTCGTGGCTCAT 1798
QY 1764 CTTTCTCTCGGAGACAGGCTTCAAGTGGCAACTCTGATTAATTACAGCATCGTCT 1823
DB 1798 ----- 1798
QY 1824 CTGGGAAACAGAGGCAAGTGAACAAAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGG 1883
DB 1799 -----GCGTTCACTTTG 1810
QY 1884 GTGCTCTGATGTTTATCTTCAAGACTTCAAGCTTTGAGAGAAATGAGAGGCTGAGCTTA 1943
DB 1811 GTGCTCTGATGTTTATCTTCAAGACTTCAAGCTTTGAGAGAAATGAGAGGCTGAGCTTA 1870

Qy	1944	TTCTGACCCCAAGTTTCTCACTCTAGTGTGAGAGCTTTGGAAAAGCTAACGTAACAAGTA	2003
Db	1871	TTCTGACCCCAAGTTTCTCACTCTAGTGTGAGAGCTTTGGAAAAGCTAACGTAACAAGTA	1930
Qy	2004	CAACCTTGGAAAACCTTGAAGTTGCAGAGCTCAGAGTTCCACCTTAAGGCAAAAGCTCTCA	2063
Db	1931	CAACCTTGGAAAACCTTGAAGTTGCAGAGCTCAGAGTTCCACCTTAAGGCAAAAGCTCTCA	1990
Qy	2064	GAAAGCTTGAAACAAGATTCTGCATTTCTGTGATCCCAAGATGTACGCCCTTGGCCAG	2123
Db	1991	GAAAGCTTGAAACAAGATTCTGCATTTCTGTGATCCCAAGATGTACGCCCTTGGCCAG	2050
Qy	2124	CAATGCTGAATTTCTTCTCTGCTTGGATCATCAAAAAAGAGTGTAAATGAAGAGAGGAG	2183
Db	2051	CAATGCTGAATTTCTTCTCTGCTTGGATCATCAAAAAAGAGTGTAAATGAAGAGAGGAG	2110
Qy	2184	CTGCTCTCCATCTTCTCTCTGAGAAAGAACTTCTCTCTCTCTCTCTCTCATGAATG	2243
Db	2111	CTGCTCTCCATCTTCTCTCTGAGAAAGAACTTCTCTCTCTCTCTCTCTCATGAATG	2170
Qy	2244	GCCTTAAGCTCAGAGAGTTGAGAACCGAGCATCCCTCCACTCAGAGTTGGGTG	2303
Db	2171	GCCTTAAGCTCAGAGAGTTGAGAACCGAGCATCCCTCCACTCAGAGTTGGGTG	2230
Qy	2304	ACGGATTTTCAACGTGGCAACCCCTTGGCCCTCACTATGAATTTTTTTCAGACCCCAAT	2363
Db	2231	ACGGATTTTCAACGTGGCAACCCCTTGGCCCTCACTATGAATTTTTTTCAGACCCCAAT	2290
Qy	2364	CTTGATCTGGAATTTGGAGTTGCTGAGACTTGGAGGCTTCTTCCCTGCTGCTTTGACTA	2423
Db	2291	CTTGATCTGGAATTTGGAGTTGCTGAGACTTGGAGGCTTCTTCCCTGCTGCTTTGACTA	2350
Qy	2424	GAAGCCGAGCTCTTAATTTTCTCAGAGCAGACTAGTGGCACTAATCCCTACCTTAAGT	2483
Db	2351	GAAGCCGAGCTCTTAATTTTCTCAGAGCAGACTAGTGGCACTAATCCCTACCTTAAGT	2410
Qy	2484	CTTCTCTCTGAGCTCCCTGAGAAAGAACTCTCTGTAATCTCTGTAAGGTTTTTGGGGATA	2543
Db	2411	CTTCTCTCTGAGCTCCCTGAGAAAGAACTCTCTGTAATCTCTGTAAGGTTTTTGGGGATA	2470
Qy	2544	AGGGTGTTTAAACAACCTCCAGGCTTCTCTTC - TTTTTTTTTTCGAAAAAAGAAAA	2602
Db	2471	AGGGTGTTTAAACAACCTCCAGGCTTCTCTTC - TTTTTTTTTTCGAAAAAAGAAAA	2530
Qy	2603	GCACACAGCACACAATTTCAAGCCATTTTCAGATCAGAACTCCAGAAAGTTCAGAAAT	2662
Db	2531	GCACACAGCACACAATTTCAAGCCATTTTCAGATCAGAACTCCAGAAAGTTCAGAAAT	2590
Qy	2663	GCCTTATCTGTAGAGTTCCCTCAGAAAGGCAATGTGTTTATGAAGAAAGTAGTAGT	2722
Db	2591	GCCTTATCTGTAGAGTTCCCTCAGAAAGGCAATGTGTTTATGAAGAAAGTAGTAGT	2650
Qy	2723	GCTCTGCGAAGAGAGCTCCCTTTAAACCTCCCTCTGTATGAAATTTCTTAAGGCTG	2782
Db	2651	GCTCTGCGAAGAGAGCTCCCTTTAAACCTCCCTCTGTATGAAATTTCTTAAGGCTG	2710
Qy	2783	AAGGATGAAGAGAGTGGGACATGTGGGTATCTTTATCCCTTTGTGTAAGCAGGAGCA	2842
Db	2711	AAGGATGAAGAGAGTGGGACATGTGGGTATCTTTATCCCTTTGTGTAAGCAGGAGCA	2770
Qy	2843	GCATGGGCTGGAGATCATAGCCCTTCTAGGCAGAATCTGTTCATCTGCCAGGCTATA	2902
Db	2771	GCATGGGCTGGAGATCATAGCCCTTCTAGGCAGAATCTGTTCATCTGCCAGGCTATA	2830
Qy	2903	GTAATTAATTAATTTTGGCAATTTGAAATATATTCGTGTGTTTTTCTTAAATGTGAAC	2962
Db	2831	GTAATTAATTAATTTTGGCAATTTGAAATATATTCGTGTGTTTTTCTTAAATGTGAAC	2890
Qy	2963	TTACCAATGAATTTTATGATCATTTCTCAGAGAGATTTTTTTTGCTCTTCTCATCTTT	3022
Db	2891	TTACCAATGAATTTTATGATCATTTCTCAGAGAGATTTTTTTTGCTCTTCTCATCTTT	2950
Qy	3023	CCAAAGTGTTCTCTGTGTGTGTGGAGCTAAGGTAAAGGGGCACTTCTGTCTGTTAA	3082

Db	2951	CCAAACAGTTCCTCCTGTTTGTGACCTAAGTAAAGAGGGACACTTCCTGCTCTGTTAA	3010
Qy	3083	CAGACAGTCATATCTGTGAGGCCAGCAAAATATTTTCTTAACTCATGGGAGACAGCAG	3142
Db	3011	CAGACAGTCATATCTGTGAGGCCAG-----	3036
Qy	3143	ATTCTTGCTTGATGAGTCAATTCCTGTGACCAATATGCTACCCCCCTGTCTTCATGCAG	3202
Db	3037	-----	3036
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US-09-949-016-5869
RESULT 15
; Sequence 5869, Application US/09949016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5869
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5869
Query Match 72.2%; Score 2679; DB 7; Length 2691;

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Best Local Similarity 100.0%; Pred. No. 0; Matches 2690; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy 1204 TAAAGACCTAGACTTCTTACAGAGATCCCTGATGATCTTTTGTGATGATGTA 1263
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Job time : 2215 secs

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GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2003, 01:53:59 ; Search time 8946 Seconds
(without alignments)
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Scoring table: IDENTITY_NTC
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Searched: 24791104 seqs, 12571243825 residues

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Minimum DB seq length: 0
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4	3690.8	99.4	4324	30 US-09-770-175-8633	Sequence 8633, Ap
5	3688	99.3	3720	76 US-60-324-185-24985	Sequence 24985, A
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25 1264.4 34.1 1727 17 US-09-396-970-8292 Sequence 8292, Ap
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27 674.4 18.2 5974 76 US-60-324-185-27323 Sequence 27323, A
28 674.4 18.2 5976 61 US-60-172-360-24780 Sequence 24780, A
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37 588.8 15.9 609 20 US-09-532-315-21032 Sequence 21032, A
38 588.8 15.9 1441 80 US-60-360-207-10718 Sequence 10718, A
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ALIGNMENTS

RESULT 1

PCT-US02-25766-9257
Sequence 9257, Application PC/TUS0225766

GENERAL INFORMATION:

APPLICANT: GENE LOGIC, INC.
APPLICANT: MUNGER, William E
APPLICANT: FAULK, Ronald
APPLICANT: SUN, Hongwei
APPLICANT: SASAI, Hiroshi
APPLICANT: WAGA, Iwao
APPLICANT: YAMAMOTO, Jun
TITLE OF INVENTION: Gene Expression Profiles in Glomerular Diseases
FILE REFERENCE: 44921-5068-WO
CURRENT APPLICATION NUMBER: PCT/US02/25766
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: US 60/311,837
PRIOR FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 13946
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 9257
LENGTH: 3713
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. U78575
PCT-US02-25766-9257

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1021 GACTTGTGCTTAATATTTATGAGCTGTGATCTGTGTGAGGAGGAGGCAAACTTCG 1080
DB 1021 GACTTGTGCTTAATATTTATGAGCTGTGATCTGTGTGAGGAGGAGGCAAACTTCG 1080
QY 1081 GATTGTGTGATGAACATCTTTTACCAAGATCGGTAAATATGATATCAATATGACT 1140
DB 1081 GATTGTGTGATGAACATCTTTTACCAAGATCGGTAAATATGATATCAATATGACT 1140
QY 1141 CAAAGCTCAACTTCAAGAGCGGCGCTTCCAGAAAGAGCGAGAAAGCTTCCAC 1200
DB 1141 CAAAGCTCAACTTCAAGAGCGGCGCTTCCAGAAAGAGCGAGAAAGCTTCCAC 1200
QY 1201 ATTTAAGACTTGAATCTTTTCAAGAGATCCCTGATGCTTTTGTGATGAGCAT 1260
DB 1201 ATTTAAGACTTGAATCTTTTCAAGAGATCCCTGATGCTTTTGTGATGAGCAT 1260
QY 1261 GTACAACGCTCTGTGAAGACCTGACAGTGAATGTTGTGCTGACAGACTCAAGAT 1320

Dh 1261 GTACAGCCTCTGTGTAAGACCCCTGACGCTGACTGTTGTGCTGACAGACTTCAGAT 1330
Qy 1321 AATGATTTACAGCCTCTGTGATGATCATATATATAGATCATGACACAGAGACCTT 1380
Dh 1321 AATGATTTACAGCCTCTGTGATGATCATATATATAGATCATGACACAGAGACCTT 1380
Qy 1381 AAGCAGTGAACACAGATCTCAGTTGATCTGAAAGACCGGCCCCCAAAAGGCTGTGA 1440
Dh 1381 AAGCAGTGAACACAGATCTCAGTTGATCTGAAAGACCGGCCCCCAAAAGGCTGTGA 1440
Qy 1441 TTCCACAGCCATGGAATTCATTCAGAGAGAGGCTGACGGGTGTGATCATGAGACTGA 1500
Dh 1441 TTCCACAGCCATGGAATTCATTCAGAGAGAGGCTGACGGGTGTGATCATGAGACTGA 1500
Qy 1501 TGACCATATGGGTGGATCCCTGCCCCGGAATGTAAGAGGGAAGGCTTGTCTTATAT 1560
Dh 1501 TGACCATATGGGTGGATCCCTGCCCCGGAATGTAAGAGGGAAGGCTTGTCTTATAT 1560
Qy 1561 TGGCATCATTTGACATTTCTACAGTCTTACAGGTTTGTAAAGAGTTGAGACACTTTGGA 1620
Dh 1561 TGGCATCATTTGACATTTCTACAGTCTTACAGGTTTGTAAAGAGTTGAGACACTTTGGA 1620
Qy 1621 AGCCTGGTACATGACGAGACACTGTCTCAGTGCATGCCAGGCTTCTAGCTGAAAG 1680
Dh 1621 AGCCTGGTACATGACGAGACACTGTCTCAGTGCATGCCAGGCTTCTAGCTGAAAG 1680
Qy 1681 GTTCAGAGGCTTCAATGACACAGATATTAAGAGATCCCTTGAAGGCTTGTCTTCTC 1740
Dh 1681 GTTCAGAGGCTTCAATGACACAGATATTAAGAGATCCCTTGAAGGCTTGTCTTCTC 1740
Qy 1741 CAAAAGTTTCGATCTGCTGATCTTCTCTCGGAGACAGGCTTCAAGTGCACACTCTG 1800
Dh 1741 CAAAAGTTTCGATCTGCTGATCTTCTCTCGGAGACAGGCTTCAAGTGCACACTCTG 1800
Qy 1801 CATTACTTACAGGATGAGTCTCTGAGGAAACAGAGGCAAGTGCACAAAGGCGA 1860
Dh 1801 CATTACTTACAGGATGAGTCTCTGAGGAAACAGAGGCAAGTGCACAAAGGCGA 1860
Qy 1861 AGTGAAGCAGGAGGCTTCACTTGTGCTGATGTTTACCTGACACTTCAACCTTGA 1920
Dh 1861 AGTGAAGCAGGAGGCTTCACTTGTGCTGATGTTTACCTGACACTTCAACCTTGA 1920
Qy 1921 GGAATCATGAGGAGGCTTCACTTGTGCTGATGTTTACCTGACACTTCAACCTTGA 1980
Dh 1921 GGAATCATGAGGAGGCTTCACTTGTGCTGATGTTTACCTGACACTTCAACCTTGA 1980
Qy 1981 TTTCGAAATGCTTAACTACAGTACAACTTGAAGAGTTGAAGTGCAGAGTCAAGTT 2040
Dh 1981 TTTCGAAATGCTTAACTACAGTACAACTTGAAGAGTTGAAGTGCAGAGTCAAGTT 2040
Qy 2041 CACCATTAAAGGAGGAGGCTTCAAGAGCTGGAACAAAGATTTGAGGCTTCTGTGATCC 2100
Dh 2041 CACCATTAAAGGAGGAGGCTTCAAGAGCTGGAACAAAGATTTGAGGCTTCTGTGATCC 2100
Qy 2101 CAAGATGACAGGCTTGTGCTGAGACATGCTGATTTCTTCTACTGTGCTCAAAAGAG 2160
Dh 2101 CAAGATGACAGGCTTGTGCTGAGACATGCTGATTTCTTCTACTGTGCTCAAAAGAG 2160
Qy 2161 GAGTGTATATAGAGTGAAGGAGGAGTGTCTCTTCATCTTCTCTGAAGAGACCTTCTC 2220
Dh 2161 GAGTGTATATAGAGTGAAGGAGGAGTGTCTCTTCATCTTCTCTGAAGAGACCTTCTC 2220
Qy 2221 TCCCTTCCCTTCTCATGATATGGGCTTGAAGGCTTGAAGAGTGAAGAGCGGAGCATCC 2280
Dh 2221 TCCCTTCCCTTCTCATGATATGGGCTTGAAGGCTTGAAGAGTGAAGAGCGGAGCATCC 2280
Qy 2281 CCTTCACCTCAGAGTGGGTGTGAGATTTTCACTGAGCAACCTTGTGCTCCACTAT 2340
Dh 2281 CCTTCACCTCAGAGTGGGTGTGAGATTTTCACTGAGCAACCTTGTGCTCCACTAT 2340
Qy 2341 TGAATTTTTTCAAGCCCCCATTTCTTCAAGTGAAGATGGAGATTTGCTGAGCTTGGCAGCT 2400
Dh 2341 TGAATTTTTTCAAGCCCCCATTTCTTCAAGTGAAGATGGAGATTTGCTGAGCTTGGCAGCT 2400

Qy 2401 TTCTTCCCTCCTGCTTGTGATGAGAACCGGACTTTAATTTCTCAGGACAGACTAGCT 2460
Dh 2401 TTCTTCCCTCCTGCTTGTGATGAGAACCGGACTTTAATTTCTCAGGACAGACTAGCT 2460
Qy 2461 GGCATTAATTCCTACTTAAGTCTTCTCTCTGACCTCTGAGAGAAATCTCTGTATCT 2520
Dh 2461 GGCATTAATTCCTACTTAAGTCTTCTCTCTGACCTCTGAGAGAAATCTCTGTATCT 2520
Qy 2521 TCTGTAAAGTTTTTGGGGATTAAGGATTTAAACCACTCCAGCTTTCTTCTTCTT 2580
Dh 2521 TCTGTAAAGTTTTTGGGGATTAAGGATTTAAACCACTCCAGCTTTCTTCTTCTT 2580
Qy 2581 TTTTTCGAAAAAGAAAAAGACACAGACACATTTCAAGCCATTTTCAGATCAGA 2640
Dh 2581 TTTTTCGAAAAAGAAAAAGACACAGACACATTTCAAGCCATTTTCAGATCAGA 2640
Qy 2641 ACTCAGAAAGTGTGACAAAGATGCTATTCGTAGAGTTCCCTCAGAAAGCCATGATGT 2700
Dh 2641 ACTCAGAAAGTGTGACAAAGATGCTATTCGTAGAGTTCCCTCAGAAAGCCATGATGT 2700
Qy 2701 TATGAAGAAAGATGATGATGCTCTGACAGAGAGCTCTCTTTAACTCTCTCT 2760
Dh 2701 TATGAAGAAAGATGATGATGCTCTGACAGAGAGCTCTCTTTAACTCTCTCTCT 2760
Qy 2761 CTTGATGAATTTCTTAAGGCTGAAGAAATGAAGAGTGGGACATGGGATATCTTATC 2820
Dh 2761 CTTGATGAATTTCTTAAGGCTGAAGAAATGAAGAGTGGGACATGGGATATCTTATC 2820
Qy 2821 CTTTTTTTAAACAGAGGAGGAGGATGGGCTGGAGATCATAGCCCTTCTAGAGCAAA 2880
Dh 2821 CTTTTTTTAAACAGAGGAGGAGGATGGGCTGGAGATCATAGCCCTTCTAGAGCAAA 2880
Qy 2881 TCCGTTCATCTGCGAGGCTATAGTAATTAATTAATTTGCAATTTGAATATATTTCTGG 2940
Dh 2881 TCCGTTCATCTGCGAGGCTATAGTAATTAATTAATTTGCAATTTGAATATATTTCTGG 2940
Qy 2941 TTGTTTTTCTAAATGTAAAGCTTAAACCAATGAATTTAGTCAATTCACAGAGAGAT 3000
Dh 2941 TTGTTTTTCTAAATGTAAAGCTTAAACCAATGAATTTAGTCAATTCACAGAGAGAT 3000
Qy 3001 TTTTTCCTCTTCTCATCTTTTCCACAGTGTCTCTGTTTGTGAGCTAAAGTAAAGA 3060
Dh 3001 TTTTTCCTCTCTCATCTTTTCCACAGTGTCTCTGTTTGTGAGCTAAAGTAAAGA 3060
Qy 3061 GGGGACACTTCTGTCTGTTTAAACAGACAGTGCATATCTGTGAGGCGCAGCAATATTTCT 3120
Dh 3061 GGGGACACTTCTGTCTGTTTAAACAGACAGTGCATATCTGTGAGGCGCAGCAATATTTCT 3120
Qy 3121 TAAATCATGGGGAGACAGAGATTTCTGCTGGTGGTGAAGTCAATGCTGAGCATATGTC 3180
Dh 3121 TAAATCATGGGGAGACAGAGATTTCTGCTGGTGGTGAAGTCAATGCTGAGCATATGTC 3180
Qy 3181 CTACCCCCCTGTCTTCAATGACAGGAGTGAATGGGGCTACATATGCTCTCTCC 3240
Dh 3181 CTACCCCCCTGTCTTCAATGACAGGAGTGAATGGGGCTACATATGCTCTCTCC 3240
Qy 3241 CCGTCTACAAAGTGTGTTTCAATGATCTTCACTCTTGTGACAGGGGAGAAAGGG 3300
Dh 3241 CCGTCTACAAAGTGTGTTTCAATGATCTTCACTCTTGTGACAGGGGAGAAAGGG 3300
Qy 3301 GGGCTGTATCTCAGGAGAGTGTGAATCTGCTTATCCCTTCTATCCCAACCTG 3360
Dh 3301 GGGCTGTATCTCAGGAGAGTGTGAATCTGCTTATCCCTTCTATCCCAACCTG 3360
Qy 3361 CCTTGAATATATGTTAGCCCATATCCCAATTAATCTGTATATTAAGACACCCAGCAG 3420
Dh 3361 CCTTGAATATATGTTAGCCCATATCCCAATTAATCTGTATATTAAGACACCCAGCAG 3420
Qy 3421 TTTTGTGCTGCTGTCTTTGTGCTGATGTTTTTAAAGAAAGAAATTTCTGTATTT 3480
Dh 3421 TTTTGTGCTGCTGTCTTTGTGCTGATGTTTTTAAAGAAAGAAATTTCTGTATTT 3480

QY	3481	TTTTCTCATATTTACTATTATTTATTTGATTTTAAAGTCTTTATTAAGGACAGAGTCTCG	3540
Db	3481	TTTTTTCATATATTTACTATTATTTGATTTTAAAGTCTTTATTAAGGACAGAGTCTCG	3540
QY	3541	TTTAGGGGTGGAGGGAATATTTCGAGGAGGCTGGGCTCTTAGGGAAGGATGGGGAAGC	3600
Db	3541	TTTAGGGGTGGAGGGAATATTTCGAGGAGGCTGGGCTCTTAGGGAAGGATGGGGAAGC	3600
QY	3601	AACATTTTTATTAAGGTCTACTATTTGGCCCTCACTTTGATTTGTTCAAGAAATGGCAATA	3660
Db	3601	AACATTTTTATTAAGGTCTACTATTTGGCCCTCACTTTGATTTGTTCAAGAAATGGCAATA	3660
QY	3661	CAATATTAAGTATATGATGTTTATATGTAATTAACCTTAAATGAGTTATTTTA	3713
Db	3661	CAATATTAAGTATATGATGTTTATATGTAATTAACCTTAAATGAGTTATTTTA	3713

RESULT 2

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US-10-003-354-3
/ Sequence 3, Application US/10003354
/ GENERAL INFORMATION:
/ APPLICANT: C. Frank Bennett
/ APPLICANT: Susan M. Freier
/ TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE
/ TITLE OF INVENTION: EXPRESSION
/ FILE REFERENCE: RTS-0348
/ CURRENT APPLICATION NUMBER: US/10/003,354
/ CURRENT FILING DATE: 2001-12-06
/ NUMBER OF SEQ ID NOS: 89
/ SEQ ID NO 3
/ LENGTH: 3713
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (401) ... (2050)
US-10-003-354-3

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Query Match	100.0%;	Score 3713;	DB 38;	Length 3713;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 3713; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	ATTTCAGGCGCGTGGTTAGAAAGACCGAGAAAGGGGCGTTCGCTCTTTGGACCTTTCA	60
		T	
Db	1	ATTTAACAGGCGCGTGGTTAGAAAGACCGAGAAAGGGGCGTTCGCTCTTTGGACCTTTTCA	60
QY	61	TGCGCTCGTTTTTTTTTCAGATGTGGCTTGGCTCGGGCGCAAGGTCCACAGCCAGCTTAA	120
Db	61	TGCGCTCGTTTTTTTTTCAGATGTGGCTTGGCTCGGGCGCAAGGTCCACAGCCAGCTTAA	120
QY	121	AGCTTACTCTTCTGTGAAAAGGGGAAAGTATCCCTGTGAAAACCGGTTAACTTTGGAG	180
Db	121	AGCTTACTCTTCTGTGAAAAGGGGAAAGTATCCCTGTGAAAACCGGTTAACTTTGGAG	180
QY	181	GGGGTCCGGGACCGTAGATTCTTCCCATGCGCAGGCGCAATGATGTGGCTTTGAGCTGTCC	240
Db	181	GGGGTCCGGGACCGTAGATTCTTCCCATGCGCAGGCGCAATGATGTGGCTTTGAGCTGTCC	240
QY	241	AGGAGCCGGCTCGACCGTGTCTGAGGGAGGCCCGGAGGGGAGGTGGCCACAGAA	300
Db	241	AGGAGCCGGCTCGACCGTGTCTGAGGGAGGCCCGGAGGGGAGGTGGCCACAGAA	300
QY	301	CGGGGTTCTGTAAAGACGTTGGGAATTCGATTTCCGAGAAGAGAAACCGGAAATT	360
Db	301	CGGGGTTCTGTAAAGACGTTGGGAATTCGATTTCCGAGAAGAGAAACCGGAAATT	360
QY	361	GAAAGAGAGCAGGCGCGTGAAGGGGAGGGGAGCTGCTAAGATGCGCTCGGCTCTCCG	420
Db	361	GAAAGAGAGCAGGCGCGCTGAAGGGGAGGGGAGCTGCTAAGATGCGGCTCTCCG	420
QY	421	GCCGTGTCTTGGGTGGTTTTTCATCTTTGATCCCGCGGCTCCCTTCTGTATCTTTGTC	480
Db	421	GCCGTGTCTTGGGTGGTTTTTCATCTTTGATCCCGCGGCTCCCTTCTGTATCTTTGTC	480

OY	481	CTGCGATCTGGAATTAAGAAGCCCATGGACATGAGGTGCTTAATGCTCTGACATGGC	540
OY	481	CTGCGATCTGGAATTAAGAAGCCCATGGACATGAGGTGCTTAATGCTCTGACATGGC	540
Db	481	CTGCGATCTGGAATTAAGAAGCCCATGGACATGAGGTGCTTAATGCTCTGACATGGC	540
OY	541	CATCAAGAAAATAGGCGCATAGAAAGTGTGATTCTCAGAGAGACAACTATATAAAAGAC	600
Db	541	CATCAAGAAAATAGGCGCATAGAAAGTGTGATTCTCAGAGAGACAACTATATAAAAGAC	600
OY	601	AACTCATAGCCTTGAAGGTGCCATCCAGTTAGGCAATTACCAACTGTGGGGAGCCT	660
Db	601	AACTCATAGCCTTGAAGGTGCCATCCAGTTAGGCAATTACCAACTGTGGGGAGCCT	660
OY	661	GAGTACCAAAACAGAGACGTGATGTCTCATGTACGAGATTTCTACGTGTGTAGAGTACTT	720
Db	661	GAGTACCAAAACAGAGACGTGATGTCTCATGTAGTCTCATGTAGAAATTTCTACGTGTGTAGAGTACTT	720
OY	721	CTTTCCAGTGAAGGAGAGCACTGACCCCTGCTCATCATACATGACTTTGTTTCAA	780
Db	721	CTTTCCAGTGAAGGAGAGCACTGACCCCTGCTCATCATACATGACTTTGTTTCAA	780
OY	781	GACCTAAGCACTGTGCTTCGCGCACTTCGCGGAGGATTTGATGATCCGCGCCGATGA	840
Db	781	GACCTAAGCACTGTGCTTCGCGCACTTCGCGGAGGATTTGATGATCCGCGCCGATGA	840
OY	841	TTACTTGTATTTCCCTCTGCAAGTGAAGCCGTGATTGAACTGTAGCTCTGAGCTAGTGG	900
Db	841	TTACTTGTATTTCCCTCTGCAAGTGAAGCCGTGATTGAACTGTAGCTCTGAGCTAGTGG	900
OY	901	TTTCCCTATTTCTAATGTGTCCAGAGACGATAGATTCATTTTAAAGACATGCCAACTAAGA	960
Db	901	TTTCCCTATTTCTAATGTGTCCAGACGATAGATTCATTTTAAAGACATGCCAACTAAGA	960
OY	961	GCGCGAATTTCTGCAAGAGCGCTTCAGAGATACATACATGAACTCAACCAAGACCTCG	1020
Db	961	GCGCGAATTTCTGCAAGAGCGCTTCAGAGATACATACATGAACTCAACCAAGACCTCG	1020
OY	1021	GACTTTGTGCTTAATTTCTAATGACTGTACTGTGTGCAAGCAGGTGGCAAGAACATTGC	1080
Db	1021	GACTTTGTGCTTAATTTCTAATGACTGTACTGTGTGCAAGCAGGTGGCAAGAACATTGC	1080
OY	1081	GATTGTGCTGATGAACAATTTTTCACAAGATCCGGTAAAAATGCAATATGACACT	1140
Db	1081	GATTGTGCTGATGAACAATTTTTCACAAGATCCGGTAAAAATGCAATATGACACT	1140
OY	1141	CAAAAGGCTCAACTTCAAAACGCGGGCTTCCAGAAAGCGAGAGAAAGCTCTTCCAC	1200
Db	1141	CAAAAGGCTCAACTTCAAAACGCGGGCTTCCAGAAAGCGAGAGAAAGCTCTTCCAC	1200
OY	1201	AATTAAGAAGCTTGAACCTTCTTAACAAGACATCCCTGATGCTCTTTTGTGATGCTGACAT	1260
Db	1201	AATTAAGAAGCTTGAACCTTCTTAACAAGACATCCCTGATGCTCTTTTGTGATGCTGACAT	1260
OY	1261	GTACAAAGCTCTCTGTAAAGACCTGCAAGGTGACTGTTTGTGCTGCAAGCTTCAAGAT	1320
Db	1261	GTACAAAGCTCTCTGTAAAGACCTGCAAGGTGACTGTTTGTGCTGCAAGCTTCAAGAT	1320
OY	1321	AATGATTAAGAGCTCTTGAATGTCAATCCATATATATAGTACATGCAACAAGAGCCTT	1380
Db	1321	AATGATTAAGAGCTCTTGAATGTCAATCCATATATATAGTACATGCAACAAGAGCCTT	1380
OY	1381	AAGCAGTGAACAAGATACAGTGAATCACTGTGAAGACCGGCGCCCCCAAAAGGCTCTGTA	1440
Db	1381	AAGCAGTGAACAAGATACAGTGAATCACTGTGAATCTGAGAGACCGGCGCCCCCAAAAGGCTCTGTA	1440
OY	1441	TTTCCAAGCCATGGAATTCATCCAGGAGAGAGCTCGACGGGTGTATCCATGAGACTGA	1500
Db	1441	TTTCCAAGCCATGGAATTCATCCAGGAGAGAGCTCGACGGGTGTATCCATGAGACTGA	1500
OY	1501	TGACCATATGGGTGGCATCCCTGCGCGGAATAGTAAAGGGGAAAAGGCTTGTGCTTTATAT	1560
Db	1501	TGACCATATGGGTGGCATCCCTGCGCGGAATAGTAAAGGGGAAAAGGCTTGTGCTTTATAT	1560

Qy 1561 TGGCATATTGACATTTCTACAGTCTTACAGGTTTGTAAAGATTGAGCACTCTTGAA 1620
Db 1561 TGGCATATTGACATTTCTACAGTCTTACAGGTTTGTAAAGATTGAGCACTCTTGAA 1620
Qy 1621 AGCCCTGGTACATGACGAGACACTGTCTCAGTGCATGCCAGGCTTCTACGCTGAACG 1680
Db 1621 AGCCCTGGTACATGACGAGACACTGTCTCAGTGCATGCCAGGCTTCTACGCTGAACG 1680
Qy 1681 GTTCAGAGGCTTCATGTCGACACAGTATTTAAGAGATTCCTTGAAAGCCTTCTCCCTC 1740
Db 1681 GTTCAGAGGCTTCATGTCGACACAGTATTTAAGAGATTCCTTGAAAGCCTTCTCCCTC 1740
Qy 1741 CAAAAGTTTCGTCTGCTCATCTTTCTCTCGGAGACAGGCTCTCAGTGGCACTCTCTG 1800
Db 1741 CAAAAGTTTCGTCTGCTCATCTTTCTCTCGGAGACAGGCTCTCAGTGGCACTCTCTG 1800
Qy 1801 CATTACTTACAGGCACTGCTCTCTGAGGAAACAGAGGCAAGTGCACAAAGGACAGA 1860
Db 1801 CATTACTTACAGGCACTGCTCTCTGAGGAAACAGAGGCAAGTGCACAAAGGACAGA 1860
Qy 1861 AGTGAGGCAAGGCTTCACCTTGCTGCTGATGTTTCTACCTGACACTCCAGCCTTGG 1920
Db 1861 AGTGAGGCAAGGCTTCACCTTGCTGCTGATGTTTCTACCTGACACTCCAGCCTTGG 1920
Qy 1921 GGAATCAGTGAAGGCTCGCCTATTCCTGACCCCAAGTTCTCAGCTCTAGTTGAGAGAC 1980
Db 1921 GGAATCAGTGAAGGCTCGCCTATTCCTGACCCCAAGTTCTCAGCTCTAGTTGAGAGAC 1980
Qy 1981 TTTTGCAATGCTTAACTACAGTACAACTTGAAAGGCTTGAAGTTGAGAGTCAAGTT 2040
Db 1981 TTTTGCAATGCTTAACTACAGTACAACTTGAAAGGCTTGAAGTTGAGAGTCAAGTT 2040
Qy 2041 CACCATTAAAGCGAAAGCCTCAGAGACCTGAAACAAGATTCGAGCCTCTGATGCC 2100
Db 2041 CACCATTAAAGCGAAAGCCTCAGAGACCTGAAACAAGATTCGAGCCTCTGATGCC 2100
Qy 2101 CAAAGTGCAGCCCTTGCCCAAGCAATGCTGAATTTCTTCTACTGCTCAAAAAG 2160
Db 2101 CAAAGTGCAGCCCTTGCCCAAGCAATGCTGAATTTCTTCTACTGCTCAAAAAG 2160
Qy 2161 GAGTGTAAATGAGTGAAGGAGGAGCTGCTCTCATCTTCTTGAGAGAAAGCCTTCTC 2220
Db 2161 GAGTGTAAATGAGTGAAGGAGGAGCTGCTCTCATCTTCTTGAGAGAAAGCCTTCTC 2220
Qy 2221 TCCCTCCCTCTCCATGAAATGAGGCTTAAGGCTCAGAGAGTTGAGAGACCGCAGACATC 2280
Db 2221 TCCCTCCCTCTCCATGAAATGAGGCTTAAGGCTCAGAGAGTTGAGAGACCGCAGACATC 2280
Qy 2281 CCTCCACTCCAGAGTGGGTGATCGGATTTCAACTGGCCAAACCTTGGCTCCACTAT 2340
Db 2281 CCTCCACTCCAGAGTGGGTGATCGGATTTCAACTGGCCAAACCTTGGCTCCACTAT 2340
Qy 2341 TGAATTTTTTCAAGCCCCCATCTTCATGCTGAAATGGAATGCTGAGCTTGAGCACT 2400
Db 2341 TGAATTTTTTCAAGCCCCCATCTTCATGCTGAAATGGAATGCTGAGCTTGAGCACT 2400
Qy 2401 TTTCTTCCCTCCGCTTGAATGAGAAACCGACCTTTAATTTCTCAGAGACAGACTACT 2460
Db 2401 TTTCTTCCCTCCGCTTGAATGAGAAACCGACCTTTAATTTCTCAGAGACAGACTACT 2460
Qy 2461 GGACATTAATCCCTACTAGTTCTTTCTCTGACTCCTGGAAGAAATCTCTGTATC 2520
Db 2461 GGACATTAATCCCTACTAGTTCTTTCTCTGACTCCTGGAAGAAATCTCTGTATC 2520
Qy 2521 TCTGTAAAGGTTTGGGGATTAAGGGGTTTAACCACTCCAGCTTCTCTCTCTTT 2580
Db 2521 TCTGTAAAGGTTTGGGGATTAAGGGGTTTAACCACTCCAGCTTCTCTCTCTTT 2580
Qy 2581 TTTTTCGAAAAAGAAAAAGCAACAGACAAATTTTCAAGCATTTTCAAGTCA 2640
Db 2581 TTTTTCGAAAAAGAAAAAGCAACAGACAAATTTTCAAGCATTTTCAAGTCA 2640
Qy 2641 ACTCAGAGTGTGACAAAGATGCTATTCGTAGAGTTCCCTCAGAAAGCATGTGT 2700

Db 2641 ACTCAGAGTGTGACAAAGATGCTATTCGTAGAGTTCCCTCAGAAAGCATGTGT 2700
Qy 2701 TATGAGAGAAAGATGATGATGCTCTGCGCAAGACAGCTCTCTTTAACTCTCTCT 2760
Db 2701 TATGAGAGAAAGATGATGATGCTCTGCGCAAGACAGCTCTCTTTAACTCTCTCT 2760
Qy 2761 CTGTAGTAATTTCTTAAAGGCTGAAGATGAAGAGAGGAGCATGAGGATCTTATC 2820
Db 2761 CTGTAGTAATTTCTTAAAGGCTGAAGATGAAGAGAGGAGCATGAGGATCTTATC 2820
Qy 2821 CTTTGTGTTAAACAGAGAGGACCATGAGGCTGAGAGATCATAGCCTTCTAGAGAA 2880
Db 2821 CTTTGTGTTAAACAGAGAGGACCATGAGGCTGAGAGATCATAGCCTTCTAGAGAA 2880
Qy 2881 TCTGTGCTACCTGCAAGGCTATGATTAATTAATTAATTTGCAATTTGAAATATCTG 2940
Db 2881 TCTGTGCTACCTGCAAGGCTATGATTAATTAATTAATTTGCAATTTGAAATATCTG 2940
Qy 2941 TTTGTTTTCTAAATGTAAGACTTAACCAATGAATTTTATGATCTTCCAGAGAGAT 3000
Db 2941 TTTGTTTTCTAAATGTAAGACTTAACCAATGAATTTTATGATCTTCCAGAGAGAT 3000
Qy 3001 TTTTGTCTCTTCATCTTTTCCAGAGTGTCTCTGTTTGTGAGCTTAAGTTAAAG 3060
Db 3001 TTTTGTCTCTTCATCTTTTCCAGAGTGTCTCTGTTTGTGAGCTTAAGTTAAAG 3060
Qy 3061 GGGGACATCTGCTGTTTAAACAGACAGTCAATCTGAGAGGCAAAATTTTCT 3120
Db 3061 GGGGACATCTGCTGTTTAAACAGACAGTCAATCTGAGAGGCAAAATTTTCT 3120
Qy 3121 TAACTCAGGGGAGACAGAGATTTGCTGCTGAGAGCATGCTGAGCATATGTC 3180
Db 3121 TAACTCAGGGGAGACAGAGATTTGCTGCTGAGAGCATGCTGAGCATATGTC 3180
Qy 3181 CTACCCCTGCTCTTCAATGACAGGAGGAGTTGAGAAATGAGGCTACATATGCTCTCC 3240
Db 3181 CTACCCCTGCTCTTCAATGACAGGAGGAGTTGAGAAATGAGGCTACATATGCTCTCC 3240
Qy 3241 CCGTCTACAAAGTGTGTTTCAATCTGATCCTTCACTGCTGAGGAGAAAGAGG 3300
Db 3241 CCGTCTACAAAGTGTGTTTCAATCTGATCCTTCACTGCTGAGGAGAAAGAGG 3300
Qy 3301 GGCTGTATCTCAGAGAGTGTGAATTCGTCTATCCCTCTCTATCCACCTG 3360
Db 3301 GGCTGTATCTCAGAGAGTGTGAATTCGTCTATCCCTCTCTATCCACCTG 3360
Qy 3361 CCTGTAAATATGTTAAGCCCAATCCCAAAATCACTGTATATTAAGACACCCCAAGCAG 3420
Db 3361 CCTGTAAATATGTTAAGCCCAATCCCAAAATCACTGTATATTAAGACACCCCAAGCAG 3420
Qy 3421 TTTGTGCTGCTGCTTGTGCTGCTGCTGCTTAAAGAGAGAAATCTTGTAT 3480
Db 3421 TTTGTGCTGCTGCTTGTGCTGCTGCTGCTTAAAGAGAGAAATCTTGTAT 3480
Qy 3481 TTTTTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3540
Db 3481 TTTTTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3540
Qy 3541 TTAGGGTGGAGGGAATTAATTAAGAGAGGCTGGCTTAAGGAGAAAGATGAGGAGC 3600
Db 3541 TTAGGGTGGAGGGAATTAATTAAGAGAGGCTGGCTTAAGGAGAAAGATGAGGAGC 3600
Qy 3601 AACATTTTAAATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3660
Db 3601 AACATTTTAAATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3660
Qy 3661 CAATATTAAGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3713
Db 3661 CAATATTAAGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3713

RESULT 3

QY 1740 CCAAAAGTTGGTCTGCTCATCTTTCTCTGGGAGAGGCTCCAGTGGCACTCT 1799
DB 1741 CCAAAAGTTGGTCTCATCTTTCTCTGGGAGAGGCTCCAGTGGCACTCTCT 1800
QY 1800 GCATTACTTACCAAGCTGGTCTCTGGGGAACAAGGCAAGTGAACAAGGAG 1859
DB 1801 GCATTACTTACCAAGCTGGTCTCTGGGGAACAAGGCAAGTGAACAAGGAG 1860
QY 1860 AAGTGGAGCCAGGCGTTCACCTTGGTCTCTGGGGAACAAGGCAAGTGAACAAGGAG 1919
DB 1861 AAGTGGAGCCAGGCGTTCACCTTGGTCTCTGGGGAACAAGGCAAGTGAACAAGGAG 1920
QY 1920 AGGAATCAGTGAAGGCTGCTGCTATCTCTGACCCCAAGTTCACCTTGAAGAGA 1979
DB 1921 AGGAATCAGTGAAGGCTGCTGCTATCTCTGACCCCAAGTTCACCTTGAAGAGA 1980
QY 1980 CTTTGGCAATGCTAATCAAGTACAACTTGGAAAGCTTGAAGTGAAGTGAAGT 2039
DB 1981 CTTTGGCAATGCTAATCAAGTACAACTTGGAAAGCTTGAAGTGAAGTGAAGT 2040
QY 2040 TCACCCATTAAGCGCAAGGCTCAGAAAGCTGGAACAAGTTCGCAATCTGTGATC 2099
DB 2041 TCACCCATTAAGCGCAAGGCTCAGAAAGCTGGAACAAGTTCGCAATCTGTGATC 2100
QY 2100 CCAAGATGTCAGCCCTTGGCCCAAGATGCTGAATTTTCTTCTAATGCTATCAAAAA 2159
DB 2101 CCAAGATGTCAGCCCTTGGCCCAAGATGCTGAATTTTCTTCTAATGCTATCAAAAA 2160
QY 2160 GGAATGTAATGAAGTGAAGGAGTGTCTCTCATCTTCTTCTGGAAGAACCTTCT 2219
DB 2161 GGAATGTAATGAAGTGAAGGAGTGTCTCTCATCTTCTTCTGGAAGAACCTTCT 2220
QY 2220 CTCTCTCTCTCTCTCTCAAGATGAGGCTTAGTCTCAGAGAGTGAAGAACGAGCATC 2279
DB 2221 CTCTCTCTCTCTCTCTCAAGATGAGGCTTAGTCTCAGAGAGTGAAGAACGAGCATC 2280
QY 2280 CCTCTCACTCAGAGTGGGAGTGAAGATTTTCACTGGCAACCTTCTCTCTCACTA 2339
DB 2281 CCTCTCACTCAGAGTGGGAGTGAAGATTTTCACTGGCAACCTTCTCTCTCACTA 2340
QY 2340 TTGAATTTTTCAGACCCCAATCTTCACTGGAATGGAGTTGCTGACCTTGGCAGC 2399
DB 2341 TTGAATTTTTCAGACCCCAATCTTCACTGGAATGGAGTTGCTGACCTTGGCAGC 2400
QY 2400 TTTCTTCTCTCTCTCTCTGAGTGAAGGAGCTTAATTTCTCTCAGACAGCTAGC 2459
DB 2401 TTTCTTCTCTCTCTCTCTGAGTGAAGGAGCTTAATTTCTCTCAGACAGCTAGC 2460
QY 2460 TGGCACAATTAATCCTTGAATCTTCTCTCTGACCTCTGGAAGTATCTCTGTAAT 2519
DB 2461 TGGCACAATTAATCCTTGAATCTTCTCTCTGACCTCTGGAAGTATCTCTGTAAT 2520
QY 2520 CTCTGTAAGGTTTGGGGAGTAAGGAGTTTAAACAATCTTCCAGCTTCTCTCTCT 2579
DB 2521 CTCTGTAAGGTTTGGGGAGTAAGGAGTTTAAACAATCTTCCAGCTTCTCTCTCT 2580
QY 2580 TTTTCTCTGAAAAAGAAAAAGACACACACACATTTTCAAGCCCTTTCAGATAG 2639
DB 2581 TTTTCTCTGAAAAAGAAAAAGACACACACACATTTTCAAGCCCTTTCAGATAG 2640
QY 2640 AACTCCAGAAAGTGTGACAAAGATGCTATGTAAGTTCCTCAGAAAGCAGTGT 2699
DB 2641 AACTCCAGAAAGTGTGACAAAGATGCTATGTAAGTTCCTCAGAAAGCAGTGT 2700
QY 2700 TTATGAAGAGAGTGTGATGCTCTGCAAGAGCTCTCTTAAATCTCTCTCTC 2759
DB 2701 TTATGAAGAGAGTGTGATGCTCTGCAAGAGCTCTCTTAAATCTCTCTCTC 2760
QY 2760 TCTTGAAGAAATTTCTTAAAGCTGAAGAGTGAAGAGTGGGAGCACTGGGGTAATCTTAT 2819
DB 2761 TCTTGAAGAAATTTCTTAAAGCTGAAGAGTGAAGAGTGGGAGCACTGGGGTAATCTTAT 2820
QY 2820 CCTTTTGTAAAAACAGAGGAGCAGTGGGCTGGAGATCATAGCCCTTCTTGGCAGA 2879

DB 2821 CCTTTTGTAAAAACAGAGGAGCAGCAGTGGGAGTGAAGTATAGCCCTTCTTGGCAGA 2880
QY 2880 ATCTGTTCATGCGCAGGCTATATGTAATTTATCTATTTTGAATTTGAATATATCTG 2939
DB 2881 ATCTGTTCATGCGCAGGCTATATGTAATTTATCTATTTTGAATTTGAATATATCTG 2940
QY 2940 GTTGTTTTCTTAATGTAAGACTTACCAATGTAATTTAGATCATCTCTCAGAGAGAT 2999
DB 2941 GTTGTTTTCTTAATGTAAGACTTACCAATGTAATTTAGATCATCTCTCAGAGAGAT 3000
QY 3000 TTTTGTGCTCTTCTCATCTTTTCAACAGTGTCTCTGTTTGTGAAGTGAAGTGAAG 3059
DB 3001 TTTTGTGCTCTTCTCATCTTTTCAACAGTGTCTCTGTTTGTGAAGTGAAGTGAAG 3060
QY 3060 AGGGAGACATCTGCTGTTTAAACAGACAGTCCATCTGAGGAGCCAGCAATATTTTC 3119
DB 3061 AGGGAGACATCTGCTGTTTAAACAGACAGTCCATCTGAGGAGCCAGCAATATTTTC 3120
QY 3120 TTAAACTCATGAGGAGACAGACAGATCTTGCCTTGTGAGGTCATCTGTCATATGT 3179
DB 3121 TTAAACTCATGAGGAGACAGACAGATCTTGCCTTGTGAGGTCATCTGTCATATGT 3180
QY 3180 CTNACCCCTCTGCTCATGAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3239
DB 3181 CTNACCCCTCTGCTCATGAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3240
QY 3240 CCGCTCTACAGAGTGTGTTTCCATCTGATCTTCCACTCTTGTCAAGGAGAGAG 3299
DB 3241 CCGCTCTACAGAGTGTGTTTCCATCTGATCTTCCACTCTTGTCAAGGAGAGAG 3300
QY 3300 GGGCTGTATCTCAGGAGATGTTGAATTCCTGTTCTATCCCTTCTATCCCACT 3359
DB 3301 GGGCTGTATCTCAGGAGATGTTGAATTCCTGTTCTATCCCTTCTATCCCACT 3360
QY 3360 GCTTGAATATGTAAGCCCATACCCCAATTAATCTGTATATTAAGACACCCCACT 3419
DB 3361 GCTTGAATATGTAAGCCCATACCCCAATTAATCTGTATATTAAGACACCCCACT 3420
QY 3420 GTTTCGCGCTCTCTTCTGCGCCATGTTTAAACAAGAGAAATCTTCTGAT 3479
DB 3421 GTTTCGCGCTCTCTTCTGCGCCATGTTTAAACAAGAGAAATCTTCTGAT 3480
QY 3480 TTTTCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3539
DB 3481 TTTTCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3540
QY 3540 GTTGAAGGAGGAGAAATTTGAAGGAGGCTGGTCTTGAAGGAGAAATGAGGAG 3599
DB 3541 GTTGAAGGAGGAGAAATTTGAAGGAGGCTGGTCTTGAAGGAGAAATGAGGAG 3600
QY 3600 CAACATTTTATTAAGTGTATCTATTTTGGCTTATCTTGTATGTTTGAAGTGGCAAT 3659
DB 3601 CAACATTTTATTAAGTGTATCTATTTTGGCTTATCTTGTATGTTTGAAGTGGCAAT 3660
QY 3660 ACAATATTAAGTGTATGTTTGAATTAATTAATTAATTAATTAATTAATTAATTAAT 3713
DB 3661 ACAATATTAAGTGTATGTTTGAATTAATTAATTAATTAATTAATTAATTAATTAAT 3714

RESULT 4
US-09-770-175-8633
Sequence 8633, Application US/09770175
GENERAL INFORMATION:
APPLICANT: Geating, David P.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
FILE REFERENCE: 1600 2058-001
CURRENT APPLICATION NUMBER: US/09/770, 175
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178, 874
PRIOR FILING DATE: 2000-01-28

NUMBER OF SEQ ID NOS: 8967
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 8633
 ; LENGTH: 4264
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-770-175-8633

Query Match 99.4%; Score 3690.8; DB 30; Length 4264;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 3706; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 ATTAACAGCCGCTGTAGAGAGACGAGAGGCGCTGCTCTTGGGACTTTTCA 60
 DB 473 ATTAACAGCCGCTGTAGAGAGACGAGAGGCGCTGCTCTTGGGACTTTTCA 532
 QY 61 TGCCCTGTTTTTTTTCAGATGTGCTGTGGGCGCAAGTCCACGACGACTTCA 120
 DB 533 TGCCCTGTTTTTTTTCAGATGTGCTGTGGGCGCAAGTCCACGACGACTTCA 592
 QY 121 AGCTTACTCTTCTGTGAAGAGGAGAAAGTATCCCTGTGAAAAGCGTTAACTTGTGAG 180
 DB 593 AGCTTACTCTTCTGTGAAGAGGAGAAAGTATCCCTGTGAAAAGCGTTAACTTGTGAG 652
 QY 181 GGGGTGCGGAGAGTGAAGTCTTCCCATGCGAGAGAGAGTGTGGCTTGAAGTGTCC 240
 DB 653 GGGGTGCGGAGAGTGAAGTCTTCCCATGCGAGAGAGAGTGTGGCTTGAAGTGTCC 712
 QY 241 AGGAGCCGCTGACGCTGTCTGAGGAGAG-CCGAGAGGCGGAGAGTGTGAGCCACAGA 299
 DB 713 AGGAGCCGCTGACGCTGTCTGAGGAGAGCCCGAGAGGCGGAGAGTGTGAGCCACAGA 772
 QY 300 ACGCGGCTTCTGTAAAGAGAGCTTGGGAAAGTTCGATTCGAGAAAGAGAAAGACCGGAT 359
 DB 773 ACGCGGCTTCTGTAAAGAGAGCTTGGGAAAGTTCGATTCGAGAAAGAGAAAGACCGGAT 832
 QY 360 TGAAGAAGAGCAGGCGCTGAGGAGGAGGAGGCTTAAGATGCGCTGCTGCTCG 419
 DB 833 TGAAGAAGAGCAGGCGCTGAGGAGGAGGAGGCTTAAGATGCGCTGCTGCTCG 892
 QY 420 GGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 479
 DB 893 GGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 952
 QY 480 CCTCAGCATCTGGAATCAAGAGACCCATGCGATCTGAGTGTGCTTATGCTGCGATGC 539
 DB 953 CCTCAGCATCTGGAATCAAGAGACCCATGCGATCTGAGTGTGCTTATGCTGCGATGC 1012
 QY 540 CCATCAAGAAATAGGCGCATAGAGTGTGATTCCTCAGAGAGAGCAACATATATAAAGA 599
 DB 1013 CCATCAAGAAATAGGCGCATAGAGTGTGATTCCTCAGAGAGAGCAACATATATAAAGA 1072
 QY 600 CAACCTCATCAGCTTGAAGAGTGCATCCATGAGGCAATTAACCAACTGTGGGAGCC 659
 DB 1073 CAACCTCATCAGCTTGAAGAGTGCATCCATGAGGCAATTAACCAACTGTGGGAGCC 1132
 QY 660 TGAAGTCAACCAAGAGGCGTGTGCTGATGAGATTTTCAACGAGTGTGAGATCT 719
 DB 1133 TGAAGTCAACCAAGAGGCGTGTGCTGATGAGATTTTCAACGAGTGTGAGATCT 1192
 QY 720 TCTTCCAGTGAAGGAGCACTGACCCCTGCTCATCACTACATGACTTTCGTTCA 779
 DB 1193 TCTTCCAGTGAAGGAGCACTGACCCCTGCTCATCACTACATGACTTTCGTTCA 1252
 QY 780 AGACTATGCACTGTGCTTCCGCTACTTCCGAGAGCTATTTGGTATCCGCGCGAGT 839
 DB 1253 AGACTATGCACTGTGCTTCCGCTACTTCCGAGAGCTATTTGGTATCCGCGCGAGT 1312
 QY 840 ATTACTTGTATTCCTGCTGAGTGAAGCGGCTGATTTGAACCTGTAGCTGTGAGTAGTG 899
 DB 1313 ATTACTTGTATTCCTGCTGAGTGAAGCGGCTGATTTGAACCTGTAGCTGTGAGTAGTG 1372
 QY 900 GTTCCCTATTTCTATGTGTCCAGGAGATGATTCATTTATTAAGACATGTCACATTAAG 959

DB 1373 GTTCCCTATTTCTATGTGTCCAGGAGATGATGATTCATTTAAGACAGTCCAACTTAAG 1432
 QY 960 AGCGGAAATTTTTCGAGAAAGCTCTTCCAGATFACATGAACTCCAAAGCAAGACCTTC 1019
 DB 1433 AGCGGAAATTTTTCGAGAAAGCTCTTCCAGATFACATGAACTCCAAAGCAAGACCTTC 1492
 QY 1020 GGAATTTGCTGCTTAATTCATGACTGTACTGTGTGAGGAGGAGTGTGCAAGACATTC 1079
 DB 1493 GGAATTTGCTGCTTAATTCATGACTGTACTGTGTGAGGAGGAGTGTGCAAGACATTC 1552
 QY 1080 GGAATTTGCTGCTTAATTCATGACTGTACTGTGTGAGGAGGAGTGTGCAAGACATTC 1139
 DB 1553 GGAATTTGCTGCTTAATTCATGACTGTACTGTGTGAGGAGGAGTGTGCAAGACATTC 1612
 QY 1140 TCAAGGCTCAACCTTCAACCGGCGCTTCCAGAAAGAGGAGGAGGAGGAGGAGGAGGAG 1199
 DB 1613 TCAAGGCTCAACCTTCAACCGGCGCTTCCAGAAAGAGGAGGAGGAGGAGGAGGAGGAG 1672
 QY 1200 CATTTAAAGACTTGAATTCCTTCAAGACATCCCTGATGCTTTTGTGATGTGACA 1259
 DB 1673 CATTTAAAGACTTGAATTCCTTCAAGACATCCCTGATGCTTTTGTGATGTGACA 1732
 QY 1260 TGTACAAAGCTCTGTGTAGAGCCCTGACGCTGACTGTTGGTGTGACAGCTTCAAGA 1319
 DB 1733 TGTACAAAGCTCTGTGTAGAGCCCTGACGCTGACTGTTGGTGTGACAGCTTCAAGA 1792
 QY 1320 TAATGATTAACGCTCTGTAAGAGCTTCAATCCATTAATTAATGATGACACAGAGGCTT 1379
 DB 1793 TAATGATTAACGCTCTGTAAGAGCTTCAATCCATTAATTAATGATGACACAGAGGCTT 1852
 QY 1380 TAAGCACTGAAAGACAGTACTCAGTTGATATCTGAAAGCCGCGCCCAAAAGGCTCTGT 1439
 DB 1853 TAAGCACTGAAAGACAGTACTCAGTTGATATCTGAAAGCCGCGCCCAAAAGGCTCTGT 1912
 QY 1440 ATTCAAGACCATGAAATTCATTCAGGAGAGAGCTGACGCGGTGTGTAACATGAGACTG 1499
 DB 1913 ATTCAAGACCATGAAATTCATTCAGGAGAGAGCTGACGCGGTGTGTAACATGAGACTG 1972
 QY 1500 ATGACATATGAGGAGGATCCCTGCGCGGAGTGTAAAGAGGAGGAGGAGGAGGAGGAGGAG 1559
 DB 1973 ATGACATATGAGGAGGATCCCTGCGCGGAGTGTAAAGAGGAGGAGGAGGAGGAGGAGGAG 2032
 QY 1560 TTGGCATATTTGATTCATGAGTCTTACAGTGTGTAAGAGTGTGAGACACTTTGGA 1619
 DB 2033 TTGGCATATTTGATTCATGAGTCTTACAGTGTGTAAGAGTGTGAGACACTTTGGA 2092
 QY 1620 AAGCCTGTGTATGATGAGAGAGCACTGTCTCAGTGTGATCCGCGAGGCTTCTAGCGTGAAC 1679
 DB 2093 AAGCCTGTGTATGATGAGAGAGCACTGTCTCAGTGTGATCCGCGAGGCTTCTAGCGTGAAC 2152
 QY 1680 GGTTCAGCGCTTATGATGAGAGAGCACTGTCTCAGTGTGATCCGCGAGGCTTCTAGCGTGAAC 1739
 DB 2153 GGTTCAGCGCTTATGATGAGAGAGCACTGTCTCAGTGTGATCCGCGAGGCTTCTAGCGTGAAC 2212
 QY 1740 CCAAAAAGTTTCGCTGTGCTCATCTTCTCTGCGGAGAGGCTCCAGTGTGCAACTTCT 1799
 DB 2213 CCAAAAAGTTTCGCTGTGCTCATCTTCTCTGCGGAGAGGCTCCAGTGTGCAACTTCT 2272
 QY 1800 GCATTTACTTACCAAGCATCGGTCTCTGGGAGACAAAGGCAAGTGAACAAAGGAGAG 1859
 DB 2273 GCATTTACTTACCAAGCATCGGTCTCTGGGAGACAAAGGCAAGTGAACAAAGGAGAG 2332
 QY 1860 AAGTGAAGCAGGCGTTCACCTTGTGCTCTGATGTTTAACTTCAAGCTTCAAGCTTTGG 1919
 DB 2333 AAGTGAAGCAGGCGTTCACCTTGTGCTCTGATGTTTAACTTCAAGCTTCAAGCTTTGG 2392
 QY 1920 AGGAATCAGTGAAGGAGCTGCTTATTCCTGACCCCAAGTTTCTACCTTGAATGAGAGA 1979
 DB 2393 AGGAATCAGTGAAGGAGCTGCTTATTCCTGACCCCAAGTTTCTACCTTGAATGAGAGA 2452
 QY 1980 CTTTCAATGTCTATCAAGTCAACCTTGAAGAGCTTGAAGTGTGACAGTCAAGT 2039


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Db 2221 CTTCTTCTCTCTCAATGATGGCCCTTAGTGCTCAGAGGTGAGGACCGCAGATC 2280
Qy 2280 CCCTCCACTCCAGAGTGGGTGGTACGGAATTTCAACTGGCCCAACCTTTGGCTCCCACTA 2339
Db 2281 CCCTCCACTCCAGAGTGGGTGGTACGGAATTTCAACTGGCCCAACCTTTGGCTCCCACTA 2340
Qy 2340 TTGAATTTTTTTTTCAGAGCCCACTTTCTTCACTGCTGGAATGGAATGCTGGAATGGCAGC 2399
Db 2341 TTGAATTTTTTTTTCAGAGCCCACTTTCTTCACTGCTGGAATGGAATGCTGGAATGGCAGC 2400
Qy 2400 TTTCTTTCCCTCTCTCTGACTAGGAACCGGACTCTTAATTTCTCAGACAGACTAGC 2459
Db 2401 TTTCTTTCCCTCTCTCTGACTAGGAACCGGACTCTTAATTTCTCAGACAGACTAGC 2460
Qy 2460 TGGCACATTTATCCCTACTTAGTTCTTTCTCTCTGACTCTCTGGAAGAAATCTCCTGTAAT 2519
Db 2461 TGGCACATTTATCCCTACTTAGTTCTTTCTCTCTGACTCTCTGGAAGAAATCTCCTGTAAT 2520
Qy 2520 CTCTGTAAGGTTTTTGGGGGATGAAGGTGTTTAAACCACTCCAGCTTTCTTCTTTT 2579
Db 2521 CTCTGTAAGGTTTTTGGGGGATGAAGGTGTTTAAACCACTCCAGCTTTCTTCTTTT 2580
Qy 2580 TTTTCTTTCTGAAAAAGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCAG 2639
Db 2581 TTTTCTTTCTGAAAAAGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCAG 2638
Qy 2640 AACTCCAGAAAGTGTGACAAAGATCCCTATTCTGAGGTTCCTCAGAAAGCCATGGTGT 2699
Db 2639 AACTCCAGAAAGTGTGACAAAGATCCCTATTCTGAGGTTCCTCAGAAAGCCATGGTGT 2698
Qy 2700 TTATGAAGAGAGATGATGATGCTCTGCGCAGAGCAGCTCTCTTTAACTCCTCCTC 2759
Db 2699 TTATGAAGAGAGATGATGATGCTCTGCGCAGAGCAGCTCTCTTTAACTCCTCCTC 2758
Qy 2760 TCTTGATGAATTTCTTAAGCTGAAGAAATCAAGAGAGTGGGATGGGTAACTTTAT 2819
Db 2759 TCTTGATGAATTTCTTAAGCTGAAGAAATCAAGAGAGTGGGATGGGTAACTTTAT 2818
Qy 2820 CCCTTTTGTAAACAGAGGAGCCATGGCTGGGAGATCATAGCCCTTCTTAGGCAGA 2879
Db 2819 CCCTTTTGTAAACAGAGGAGCCATGGCTGGGAGATCATAGCCCTTCTTAGGCAGA 2878
Qy 2880 ATCTGTTCTACTGCGAGCTATAGTAATTAATTAATTTTGAATTTGAATATATTTCTG 2939
Db 2879 ATCTGTTCTACTGCGAGCTATAGTAATTAATTAATTTTGAATTTGAATATATTTCTG 2938
Qy 2940 GTTGTTTTTCTTAATGTGAAGCTTACCAATGAATTTTGAATCATTTCTCAGAGGAT 2999
Db 2939 GTTGTTTTTCTTAATGTGAAGCTTACCAATGAATTTTGAATCATTTCTCAGAGGAT 2998
Qy 3000 TTTTCTTTGCTCTCTCACTTTTCCAAAGTGTCTCTCTGTTGTGAGCTAAGGTAAAG 3059
Db 2999 TTTTCTTTGCTCTCTCACTTTTCCAAAGTGTCTCTCTGTTGTGAGCTAAGGTAAAG 3058
Qy 3060 AGGGGACATTTCTGCTGTGTTTAAACAGACAGTCCATATCTGTGAGGCGCAGCAATATTTTC 3119
Db 3059 AGGGGACATTTCTGCTGTGTTTAAACAGACAGTCCATATCTGTGAGGCGCAGCAATATTTTC 3118
Qy 3120 TTAACCTCATGGGGAGACAGCATTTCTGCTTGGTGGGTCAATGCTGTGCCATATGT 3179
Db 3119 TTAACCTCATGGGGAGACAGCATTTCTGCTTGGTGGGTCAATGCTGTGCCATATGT 3178
Qy 3180 CCTACCCCTCTCTCTCATGAGGGAAGTTGGAATGGGGGCTACATATGCCCTCTCTCTC 3239
Db 3179 CCTACCCCTCTCTCTCATGAGGGAAGTTGGAATGGGGGCTACATATGCCCTCTCTCTC 3238
Qy 3240 CCGCTTACAAGAGTGTGTTTCCATCTGATCTCTTCCATCTCTTGTGAGGGGAAGAAG 3299
Db 3239 CCGCTTACAAGAGTGTGTTTCCATCTGATCTCTTCCATCTCTTGTGAGGGGAAGAAG 3298
Qy 3300 GGGCTGGTATCTCAGGCAGATTTGTAATTTCTGTTCTATCCCTTCTCTATCCACCT 3359
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Db 3299 GGGCTGGTATCTCAGGCAGATTTGTAATTTCTGTTCTATATCCCTTCTATATCCACCT 3358
Qy 3360 GCCTTGATATATGTTAGCCCATACCCCAATAAATAACTGTCTATATAGACACCCCCAGCCA 3419
Db 3359 GCCTTGATATATGTTAGCCCATACCCCAATAAATAACTGTCTATATAGACACCCCCAGCCA 3418
Qy 3420 GTTCTGGCTGCCCTGTCTTGTGCTGCCATGTTTTCACAGAAAGAAATTTCTTGTCTAT 3479
Db 3419 GTTCTGGCTGCCCTGTCTTGTGCTGCCATGTTTTCACAGAAAGAAATTTCTTGTCTAT 3478
Qy 3480 TTTTCTTTTTCATATATTTTACTATTTATGATGATTTAATTAAGTGTGTTTATTAAGCAGAGTTCT 3539
Db 3479 TTTTCTTTTTCATATATTTTACTATTTATGATGATTTAAGTGTGTTTATTAAGCAGAGTTCT 3538
Qy 3540 GTTAGGGGTGGGAGGAAATATTTAGGGAGGGCTGGGTCTTTAGGGAAAGAAATGGGGAAG 3599
Db 3539 GTTAGGGGTGGGAGGAAATATTTAGGGAGGGCTGGGTCTTTAGGGAAAGAAATGGGGAAG 3598
Qy 3600 CAACATTTTATTAAGTGTACTATTTTGGCTCTACTTTTGTATTTGTTAGAAATGGCAAT 3659
Db 3599 CAACATTTTATTAAGTGTACTATTTTGGCTCTACTTTTGTATTTGTTAGAAATGGCAAT 3658
Qy 3660 ACAATATAAAGTGATATATGTTTAAATGTAATAAATTTAATGATTTATTTA 3713
Db 3659 ACAATATAAAGTGATATATGTTTAAATGTAATAAATTTAATGATTTATTTA 3712

RESULT 6
US-09-667-228-736
; Sequence 736, Application US/09667228
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1196-001
; CURRENT APPLICATION NUMBER: US/09/667,228
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/154,931
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 736
; LENGTH: 4266
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-667-228-736

Query Match 99.1%; Score 3678.4; DB 26; Length 4266;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3712; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

Qy 1 ATTAACAGCCGCTGTTAGGAGGACGAGAGGGGGCTTCGCTCTTTGGGACTTTTCA 60
Db 473 ATTAACAGCCGCTGTTAGGAGGACGAGAGGGGGCTTCGCTCTTTGGGACTTTTCA 532
Qy 61 TGCCTCGTTTTTTTTTTCAGATGTGGCTTGTCTGGGCGCAAGTCCAGCAGCCAGCTTA 120
Db 533 TGCCTCGTTTTTTTTTTCAGATGTGGCTTGTCTGGGCGCAAGTCCAGCAGCCAGCTTA 592
Qy 121 AGCTTACTCTCTCTGTAAGGGGAAAGTATCCCTCTGGAAGCGGTAACTTTGTGGAG 180
Db 593 AGCTTACTCTCTCTGTAAGGGGAAAGTATCCCTCTGGAAGCGGTAACTTTGTGGAG 652
Qy 181 GGGGTGGGGAGCGTGAATTTCTCCCATGCCAGGCGAATGGTGTGGCTTGAAGTGTCC 240
Db 653 GGGGTGGGGAGCGTGAATTTCTCCCATGCCAGGCGAATGGTGTGGCTTGAAGTGTCC 712
Qy 241 AGAGCCGGCTCGACGTGCTGAGGGAGG-CCCGAGGGGGGGGGAGGTGGCCCAAGA 299
Db 713 AGAGCCGGCTCGACGTGCTGAGGGAGGCCCCCGAGGGGGGGAGGTGGCCCAAGA 772
Qy 300 ACGCGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCGAGAGAGGAAGAACCGGAT 359
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||||| 773 ACGGGTTCTGTAAAGAGCGTTGGGAGATTCGATTCGAGAGAGGAGAACCGGAT 832
QY 360 TGAAGAGAGCCAGCGCGCTGAGGGGAGGGGCTGCTAAGATGGCGTCCGCTCTCCG 419
Db 833 TGAAGAGAGCCAGCGCGCTGAGGGGAGGGGCTGCTAAGATGGCGTCCGCTCTCCG 892
QY 420 GCGCGTCTGTTGGTGGTCTTTCATCTTTGATCCCGGGTCCCTTCTGTTACCTTGT 479
Db 893 GCGCGTCTGTTGGTGGTCTTTCATCTTTGATCCCGGGTCCCTTCTGTTACCTTGT 952
QY 480 CCTCAGCATCTGGAATCAAGAGACCCATGSCATCTGAGGTGCCTTATGCTCTGCGATGC 539
Db 953 CCTCAGCATCTGGAATCAAGAGACCCATGSCATCTGAGGTGCCTTATGCTCTGCGATGC 1012
QY 540 CCATCAAGAAAATAGGCCATAGAGTGTGATTCCTCAGGAGAGACAAATATAAAAAGA 599
Db 1013 CCATCAAGAAAATAGGCCATAGAGTGTGATTCCTCAGGAGAGACAAATATAAAAAGA 1072
QY 600 CAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTTACCACACTGTGGGAGCC 659
Db 1073 CAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTTACCACACTGTGGGAGCC 1132
QY 660 TGAGTACCACAAACAGAGCGTGCATCTCTCATGCAAGATTTCTAGCTGGTTGAGAGTATCT 719
Db 1133 TGAGTACCACAAACAGAGCGTGCATCTCTCATGCAAGATTTCTAGCTGGTTGAGAGTATCT 1192
QY 720 TCTTTCCAGTGAAGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCA 779
Db 1193 TCTTTCCAGTGAAGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCA 1252
QY 780 AGACTATGCACTGTTCCTTCGCTTCCGCTACTTCCGGAGCTATTTGGTATCCGGCCCATG 839
Db 1253 AGACTATGCACTGTTCCTTCGCTTCCGCTACTTCCGGAGCTATTTGGTATCCGGCCCATG 1312
QY 840 ATTACTTGTATTCCTCTGCACTGAGCGCTGATTTGAATCTGTAGCTCTGGAGCTAGTG 899
Db 1313 ATTACTTGTATTCCTCTGCACTGAGCGCTGATTTGAATCTGTAGCTCTGGAGCTAGTG 1372
QY 900 GTTCCCTATTCATGTGTCAGGAGCGATGAGTTCAATTAAGACAGTCCAAATGAAG 959
Db 1373 GTTCCCTATTCATGTGTCAGGAGCGATGAGTTCAATTAAGACAGTCCAAATGAAG 1432
QY 960 AGCGGAATTTCTCAGAGAGCTGCTCCAGGATACATCAACCTCAACAGAACCTC 1019
Db 1433 AGCGGAATTTCTCAGAGAGCTGCTCCAGGATACATCAACCTCAACAGAACCTC 1492
QY 1020 GGACTTTGCTGCTAAATTTCTATGGACTGTACTGTGTGACGAGGTGGCAAGAACATTC 1079
Db 1493 GGACTTTGCTGCTAAATTTCTATGGACTGTACTGTGTGACGAGGTGGCAAGAACATTC 1552
QY 1080 GGAATGTGGTGATGAACAAATCTTTTCAAGATCGGTAAAAATGATATGAATGACC 1139
Db 1553 GGAATGTGGTGATGAACAAATCTTTTCAAGATCGGTAAAAATGATATGAATGACC 1612
QY 1140 TCARAAGGTCAACCTACAAACGGCGGCTCCCAAGAGAGCGAGAGCGCTCTTCCCA 1199
Db 1613 TCARAAGGTCAACCTACAAACGGCGGCTCCCAAGAGAGCGAGAGCGCTCTTCCCA 1672
QY 1200 CATTTAAAGACCTAGACTCTTTTACAAGACATCCCTGATGGTCTTTTGTGATGCTGACA 1259
Db 1673 CATTTAAAGACCTAGACTCTTTTACAAGACATCCCTGATGGTCTTTTGTGATGCTGACA 1732
QY 1260 TGTACAAACCTCTGTGAAGACCTGACGCTGACTGTTGGTCTGAGAGCTTCAAGA 1319
Db 1733 TGTACAAACCTCTGTGAAGACCTGACGCTGACTGTTGGTCTGAGAGCTTCAAGA 1792
QY 1320 TAATGATTTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAAACAGAGCCCT 1379
Db 1793 TAATGATTTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAAACAGAGCCCT 1852
QY 1380 TAAGCAGTGAACACAGTACTCAGTTGATCTCGAAGACCGGCCCCCAAGAGGCTCTGT 1439

Db 1853 TAAGCAGTGAACACAGTACTCAGTTGATCTCGAAGACCGGCCCCCAAGAGGCTCTGT 1912
QY 1440 ATTCCACAGCCATCGAATCCATCCAGGAGAGGCTCCGACGGGTGGTACCATGAGACTG 1499
Db 1913 ATTCCACAGCCATCGAATCCATCCAGGAGAGGCTCCGACGGGTGGTACCATGAGACTG 1972
QY 1500 ATGACCATATGGGTGGCATCCCTCGCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 1559
Db 1973 ATGACCATATGGGTGGCATCCCTCGCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 2032
QY 1560 TTGGCATCATTTGACATTTCTACAGTCTTACAGTTTGTAAAGTTTGAGGACACTCTTGA 1619
Db 2033 TTGGCATCATTTGACATTTCTACAGTCTTACAGTTTGTAAAGTTTGAGGACACTCTTGA 2092
QY 1620 AAGCCCTGTTACATCAGCGAGACACTGTCTCAGTGCATCGCCAGGCTTCTACGCTGAAC 1679
Db 2093 AAGCCCTGTTACATCAGCGAGACACTGTCTCAGTGCATCGCCAGGCTTCTACGCTGAAC 2152
QY 1680 GGTTCAGCGCTTCATGTGCAACACAGATTTAAAGAGATTCCTTTGAAGCCTTCTCCTT 1739
Db 2153 GGTTCAGCGCTTCATGTGCAACACAGATTTAAAGAGATTCCTTTGAAGCCTTCTCCTT 2212
QY 1740 CCAAAAAGTTTCGGTCTGCTCATCTTCTCGCGGAGAGGCTCCAGTGGCAACTCT 1799
Db 2213 CCAAAAAGTTTCGGTCTGCTCATCTTCTCGCGGAGAGGCTCCAGTGGCAACTCT 2272
QY 1800 GCATTTACTTTACCAGCATCGGTCTCTGGGGAACACAAAGGCAAGTGAACAAAGGAG 1859
Db 2273 GCATTTACTTTACCAGCATCGGTCTCTGGGGAACACAAAGGCAAGTGAACAAAGGAG 2332
QY 1860 AAGTGGAGCAGCGGTTCACTTGGTCTGCTGATGTTTAACTTCTCAGACTCCACCTTTGG 1919
Db 2333 AAGTGGAGCAGCGGTTCACTTGGTCTGCTGATGTTTAACTTCTCAGACTCCACCTTTGG 2392
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Db 2393 AGGAATTCAGTGGGCTCGCTATTCCTGACCCAGTTTCTCACTCTAGTTGGAGAGA 2452
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Db 2453 CTTTGCATAATGCTTAATAAGTACAACTTCGAAAGCTTGAAGTTGCAGAGTCAGAGT 2512
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Db 2573 CBAAGATGTCAGCCCTTGGCCCGAGCAATGCTGAATTTTCTTCTACTTGTCTCATCAAAAA 2632
QY 2160 GGAATGTAATAGAAAGTGAAGGAGCTGCTCCTCCATCTTCTTCGAAGAAACCTTCT 2219
Db 2633 GGAATGTAATAGAAAGTGAAGGAGCTGCTCCTCCATCTTCTTCGAAGAAACCTTCT 2692
QY 2220 CTCCTTCTCTTCTCATGAATGGGCTTAGTGCTTCAGAGAGTTGAGGACCGCAGATC 2279
Db 2693 CTCCTTCTCTTCTCATGAATGGGCTTAGTGCTTCAGAGAGTTGAGGACCGCAGATC 2752
QY 2280 CCTTCACCTCCAGAGTTGGGTGAGGATTTTCACTGSCCAACCTTTGCTCCACTA 2339
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QY 2400 TTTCTTTTCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCTCCTCAGCAGACTAGC 2459
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RESULT 8

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US-09-726-802-2146
; Sequence 2146, Application US/09726802
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Palb, Dean A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USBS
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; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2025-001
; CURRENT APPLICATION NUMBER: US/09/726,802
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/168,012
; PRIOR FILING DATE: 1999-11-30
; NUMBER OF SEQ ID NOS: 2872
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2146
; LENGTH: 4266
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-726-802-2146
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Query Match 99.1%; Score 3678.4; DB 29; Length 4266;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3712; Conservative 0; Mismatches 1; Indels 3; Gaps 3;
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DB 3893 CAGTTCTGCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3952
QY 3478 ATTATTTTTCATAAATTTACTATTTATGATGATTTTAAAGTGTGTTTATTAAGGACAGAGTT 3537
DB 3953 ATTATTTTTCATAAATTTACTATTTATGATGATTTTAAAGTGTGTTTATTAAGGACAGAGTT 4012
QY 3538 CTGTTAGGGGTGGGAGGGAATATTTAGGAGGAGGCTGGGCTTTAGGCAAGGAATGGGA 3597
DB 4013 CTGTTAGGGGTGGGAGGGAATATTTAGGAGGAGGCTGGGCTTTAGGCAAGGAATGGGA 4072
QY 3598 AGCAACATTTTATTAAGTGTACTATTTGCTCTACTTTGCTATGTTGTTAGAAATGGCAA 3657
DB 4073 AGCAACATTTTATTAAGTGTACTATTTGCTCTACTTTGCTATGTTGTTAGAAATGGCAA 4132
QY 3658 ATCAATATATAAGTGATATATGTTTAAATGTAATAAATCTTTAATGAGTTATTTA 3713
DB 4133 ATCAATATATAAGTGATATATGTTTAAATGTAATAAATCTTTAATGAGTTATTTA 4188
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RESULT 10

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US-60-278-258-4040
; Sequence 4040, Application US/60278258
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide
; FILE REFERENCE: Polymorphisms Identified Thereby
; FILE REFERENCE: GX-0010-1 P
; CURRENT APPLICATION NUMBER: US/60/278,258
; NUMBER OF SEQ ID NOS: 17730
; SOFTWARE: PERL Program
; SEQ ID NO 4040
; LENGTH: 3732
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 348086.4
US-60-278-258-4040
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Query Match 98.7%; Score 3665.4; DB 71; Length 3732;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3711; Conservative 0; Mismatches 1; Indels 4; Gaps 4;
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QY 1 ATTAAACAGGCGGTGGTTAGGAAGACGAGAGAGGGGCTTCGCTCCCTTTGGGACTTTTCA 60
DB 11 ATTAAACAGGCGGTGGTTAGGAAGACGAGAGAGGGGCTTCGCTCCCTTTGGGACTTTTCA 70
QY 61 TGCTCGTTTTTTTTTTCAGATGTGGCTTGTGCTGGGCGCAAGGTCCAGCAGCAGCAGCTTA 120
DB 71 TGCTCGTTTTTTTTTTCAGATGTGGCTTGTGCTGGGCGCAAGGTCCAGCAGCAGCAGCTTA 130
QY 121 AGCTTACTCTTCTGTGAAAGGGAAGTATCCCTGTGGAAGCGGTAAACTTTGGAG 180
DB 131 AGCTTACTCTTCTGTGAAAGGGAAGTATCCCTGTGGAAGCGGTAAACTTTGGAG 190
QY 181 GGGGTGGGACGAGTCTCTCCCATGCCAGGCAATGCTGTGGCTTGGCTGCTGCTCC 240
DB 191 GGGGTGGGACGAGTCTCTCCCATGCCAGGCAATGCTGTGGCTTGGCTGCTGCTCC 250
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QY 241 AGAGAGCGGCTCGACGTGTTCTGAGGGAGG--CCCGAGGGGGCGGGAGGTGGGCCACAGA 299
DB 251 AGAGAGCGGCTCGACGTGTTCTGAGGGAGGCGCCCGAGGGGGCGGGAGGTGGGCCACAGA 310
QY 300 ACCGGGTTCTGTAAAGAGACGTTGGGAGATTCGATTCGAGAGAGGAGAACCGGAT 359
DB 311 ACCGGGTTCTGTAAAGAGACGTTGGGAGATTCGATTCGAGAGAGGAGAACCGGAT 370
QY 360 TGAAGAGAGCCAGGCGCTGAGGGGGAGGGGCTGCTAAGATGGGCTCGGCTCTCTCCG 419
DB 371 TGAAGAGAGCCAGGCGCTGAGGGGGAGGGGCTGCTAAGATGGGCTCGGCTCTCTCCG 430
QY 420 GGGCGTCTCTTCGGTCCGTTTTTCATCTTTGATCCCGGGTCCCTTCCTGACCTTGT 479
DB 431 GGGCGTCTCTTCGGTCCGTTTTTCATCTTTGATCCCGGGTCCCTTCCTGACCTTGT 490
QY 480 CCTCAGCATCTGGAATCAAGAGACCCAT--GGCATCTGAGGTGCTTATGCTCTGGCATG 538
DB 491 CCTCAGCATCTGGAATCAAGAGACCCATGAGGTCATCTGAGGTGCTTATGCTCTGGCATG 550
QY 539 CCCAT--CAAGAAATAGGCCATAGAAAGTGTGATTCCTCAGAGAGAGACAATATAAAA 597
DB 551 CCCATCAAGAAATAGGCCATAGAAAGTGTGATTCCTCAGAGAGAGACAATATAAAA 610
QY 598 GACAACTCATAGCCTTGAAAGGTGCATCCAGTTAGGCATTAACCACTGTGGGAG 657
DB 611 GACAACTCATAGCCTTGAAAGGTGCATCCAGTTAGGCATTAACCACTGTGGGAG 670
QY 658 CTGAGTACCAACACAGAGGCTGATGTCCTCATGCAAGATTTCTACGTGTTGAGATAT 717
DB 671 CTGAGTACCAACACAGAGGCTGATGTCCTCATGCAAGATTTCTACGTGTTGAGATAT 730
QY 718 CTTCTTTCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACATTTCTGTT 777
DB 731 CTTCTTTCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACATTTCTGTT 790
QY 778 CAAGACTATGACCTGTTGCTTCCCTGCTACTTCCGGAGCTATTTGGTATCCGGCCCA 837
DB 791 CAAGACTATGACCTGTTGCTTCCCTGCTACTTCCGGAGCTATTTGGTATCCGGCCCA 850
QY 838 TGATTTACTTGTATTCCTCTGAGTGAGCGGCTGATGAATCTGTAGCTCTGGAGCTAG 897
DB 851 TGATTTACTTGTATTCCTCTGAGTGAGCGGCTGATGAATCTGTAGCTCTGGAGCTAG 910
QY 898 TGGTTCCTTATCTATGTGTCCAGCGACGATGATTCATTATTAAGACAGCTCCAAATAA 957
DB 911 TGGTTCCTTATCTATGTGTCCAGCGACGATGATTCATTATTAAGACAGCTCCAAATAA 970
QY 958 AGAGCGGAATTTCTCAGAAAGTCTTCCAGGATCTACATGAACCTCAACAGAACCC 1017
DB 971 AGAGCGGAATTTCTCAGAAAGTCTTCCAGGATCTACATGAACCTCAACAGAACCC 1030
QY 1018 TCGGACTTTGCTGCTTAAATTTCTATGACTGTACTGTGTCAGGCGAGGTGGCAAGACAT 1077
DB 1031 TCGGACTTTGCTGCTTAAATTTCTATGACTGTACTGTGTCAGGCGAGGTGGCAAGACAT 1090
QY 1078 TCGGATTTGCTGATCAACAACTCTTTTACCAAGATCGTTAAATAATGCATATCAATATGA 1137
DB 1091 TCGGATTTGCTGATCAACAACTCTTTTACCAAGATCGTTAAATAATGCATATCAATATGA 1150
QY 1138 CTTCAAAGGCTCAACCTCAAAACGGCGGCTTCCAGAAAGAGCGAGAGAGCTCTTTC 1197
DB 1151 CTTCAAAGGCTCAACCTCAAAACGGCGGCTTCCAGAAAGAGCGAGAGAGCTCTTTC 1210
QY 1198 CACTTTAAAGACTAGACTTTCTTAACAAGATCCCTGTATGCTCTTTTGTGATGTGA 1257
DB 1211 CACTTTAAAGACTAGACTTTCTTAACAAGATCCCTGTATGCTCTTTTGTGATGTGA 1270
QY 1258 CAGTACAAAGCTCTCTGTAAAGACCCCTGAGCGTACTGTTTGGTGTGTCAGAGCTTCAA 1317
DB 1271 CAGTACAAAGCTCTCTGTAAAGACCCCTGAGCGTACTGTTTGGTGTGTCAGAGCTTCAA 1330
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Qy	1318	GATAATGGGATTACAGCCTCTTGATGTCAAATCCATAATATAGATCATGCAACAAGAGCC	1377
Db	1331	GATTAATGGGATTATAGCCTCTTGATGTCAAATCCATAATATAGATCATGCAACAAGAGCC	1390
Qy	1378	CTTTAAGCAGTGAAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAGAGCTCT	1437
Db	1391	CTTTAAGCAGTGAAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAGAGCTCT	1450
Qy	1438	GTATTCCACAGCATGGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGAC	1497
Db	1451	GTATTCCACAGCCATGGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGAC	1510
Qy	1498	TGATGACATATGGGTGGGATCCCTGCCCGGAATAGTATAAGGGGAAAGGCTTCGCTTTA	1557
Db	1511	TGATGACATATGGGTGGGATCCCTGCCCGGAATAGTATAAGGGGAAAGGCTTCGCTTTA	1570
Qy	1558	TATTGGCATCATTGACATTTACAGTCTTTACAGGTTTGTTAAGAAAGTTGGAGCACTCTTG	1617
Db	1571	TATTGGCATCATTGACATTTACAGTCTTTACAGGTTTGTTAAGAAAGTTGGAGCACTCTTG	1630
Qy	1618	GAAGAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCAATCGGCCAGGCTTCTACGCTGA	1677
Db	1631	GAAGAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCAATCGGCCAGGCTTCTACGCTGA	1690
Qy	1678	ACGGTTCACGGCTTCATGTCGCAACACAGTATTTAAGAAAGTTTCCCTTGAAGCCTTCTCC	1737
Db	1691	ACGGTTCACGGCTTCATGTCGCAACACAGTATTTAAGAAAGTTTCCCTTGAAGCCTTCTCC	1750
Qy	1738	TTCCAAAAGTTTTCGGTCCTGGCTCATCTTTCTCTCGCGAGCAGGCTCCAGTGGCAACTC	1797
Db	1751	TTCCAAAAGTTTTCGGTCCTGGCTCATCTTTCTCTCGCGAGCAGGCTCCAGTGGCAACTC	1810
Qy	1798	CTGCATTTACTTACAGCGATCGGTCTCTGGGGACACAAAGGCACAAGTGCACAAAGAGC	1857
Db	1811	CTGCATTTACTTACAGCGATCGGTCTCTGGGGACACAAAGGCACAAGTGCACAAAGAGC	1870
Qy	1858	AGAAAGTCGAGCCAGGGGTTCACTCTTGTCGTCTCTGATGTTTATCCTCAGACTCCACCTTT	1917
Db	1871	AGAAAGTCGAGCCAGGGGTTCACTCTTGTCGTCTCTGATGTTTATCCTCAGACTCCACCTTT	1930
Qy	1918	GGAGAAATCAGTGAGGGTCGGCTATTCTCGACCCAGTTTCTCAGCTTAGTTCGAGA	1977
Db	1931	GGAGAAATCAGTGAGGGTCGGCTATTCTCGACCCAGTTTCTCAGCTTAGTTCGAGA	1990
Qy	1978	GACTTTGCAATGCTAACTACAAGTACAACCTTGCGAAAAGCTTGAAGTTGCAGAGTCAGA	2037
Db	1991	GACTTTGCAATGCTAACTACAAGTACAACCTTGCGAAAAGCTTGAAGTTGCAGAGTCAGA	2050
Qy	2038	GTTCAACCATTAAGCGCAAAAGCCTCAGAGAAGCTCGGAACAAGATTCGCCATCTCTGTGA	2097
Db	2051	GTTCAACCATTAAGCGCAAAAGCCTCAGAGAAGCTCGGAACAAGATTCGCCATCTCTGTGA	2110
Qy	2098	TCCCAAGATTCAGCCCTTCGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCAATCAAAA	2157
Db	2111	TCCCAAGATTCAGCCCTTCGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCAATCAAAA	2170
Qy	2158	AAGGAGTGTAATAGAAGTGAGGGAGCTGCTCCTCCATCTTTCTCTGAAGAAGAACCTT	2217
Db	2171	AAGGAGTGTAATAGAAGTGAGGGAGCTGCTCCTCCATCTTCTTCTGAAGAAGAACCTT	2230
Qy	2218	CTCTCCTTCTCTTCTTCATGAATGGGCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCA	2277
Db	2231	CTCTCCTTCTCTTCTTCATGAATGGGCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCA	2290
Qy	2278	TCCCTCCACCTCCAGAGTTGGGTGGTACGGAATTTCAACTGGCCAAACCTTTTGCCTCCAC	2337
Db	2291	TCCCTCCACCTCCAGAGTTGGGTGGTACGGAATTTCAACTGGCCAAACCTTTTGCCTCCAC	2350
Qy	2338	TATTGAATTTTTTTTTCAGACCCCACTTCTTCATGCTGGAAATGGGATTCGCTGAATGGCA	2397
Db	2351	TATTGAATTTTTTTTTCAGACCCCACTTCTTCATGCTGGAAATGGGATTCGCTGAATGGCA	2410
Qy	2398	GCCTTTCTTTCCCTCTGCTTTTGATAGGAAACCGGACTCTTAATTTTCTCAGGACAGACTA	2457

D	b	2411	GCTTTCTTTCCCTCGTCTTTTGACTAGAACCGACCTTTAAATTTCTCAGGACGACTA	2470
Q	y	2458	GCTGGCACATTATCCCTACCTTAGTTCTTTCTCTCACTCTCGGAAGAATACTCTGTGA	2517
D	b	2471	GCTGGCACATTATCCCTACCTTAGTTCTTTCTCTGACTCCTGGGAAGAATACCTCTGTA	2530
Q	y	2518	ATCTCTGTAAAAGTTTTTGGGGGATAGGGTGTTTAAACCCTCCCAGCTTTCTCTCTCT	2577
D	b	2531	ATCTCTGTAAAAGTTTTTGGGGGATAGGGTGTTTAAACCCTCCCAGCTTTCTCTCTCT	2590
Q	y	2578	TTTTTTTTTCTGAAAAAGAAAAAGCACAGCACACAATTTCAAGCCAAATTTTCAGATC	2637
D	b	2591	TTTTTTTTTCTGAAAAAG - AAAGCACACAGCACACAATTTCAAGCCAAATTTTCAGATC	2649
Q	y	2638	AGAACTCCAGAGTGTTGACAAGATGCCTATTCTGTAGAGTTCCCTCAGAGAGCCATGCT	2697
D	b	2650	AGAACTCCAGAGTGTTGACAAGATGCCTATTCTGTAGAGTTCCCTCAGAGAGCCATGCT	2709
Q	y	2698	GTTATTGAGAGAGATGATGATTGCTCTGCCAGAGACAGCTCCTCTTTAAACTCTCTCC	2757
D	b	2710	GTTATTGAGAGAGATGATGATTGCTCTGCCAGAGACAGCTCCTCTTTAAACTCTCTCC	2769
Q	y	2758	TCTCTTGATGAATTTCTTAAGCCTCAAGGAATGAAGAGATGGGACATGGGGTAATCTTT	2817
D	b	2770	TCTCTTGATGAATTTCTTAAGCCTCAAGGAATGAAGAGATGGGACATGGGGTAATCTTT	2829
Q	y	2818	ATCCCTTTTGTAAACACAGGACGACCATGGCTGGGAGATCATAGCCCTCTCTAGGCA	2877
D	b	2830	ATCCCTTTTGTAAACACAGGACGACCATGGCTGGGAGATCATAGCCCTCTCTAGGCA	2889
Q	y	2878	GAATCCTGTTCACTGCGCAGGCTATAGTAATATTACTAATTTTGCAATTTGAAATATATTC	2937
D	b	2890	GAATCCTGTTCACTGCGCAGGCTATAGTAATATTACTAATTTTGCAATTTGAAATATATTC	2949
Q	y	2938	TGGTTGTTTTTCTAAATGTGAGACATTACCAAATGCAATTTTAGATCATCTCCAGAGGAG	2997
D	b	2950	TGGTTGTTTTTCTAAATGTGAGACATTACCAAATGCAATTTTAGATCATCTCCAGAGGAG	3009
Q	y	2998	ATTTTTTTTTGCTCTCTCATCTTTTTCCAACAGTGTTCTCTGTTGTGGAGCTAAGGTAA	3057
D	b	3010	ATTTTTTTTTGCTCTCTCATCTTTTTCCAACAGTGTTCTCTGTTGTGGAGCTAAGGTAA	3069
Q	y	3058	AGAGGGACACTTCTGTCTGTTTACAGACAGTCCATATCTGTGAGGCCACGCAATATTT	3117
D	b	3070	AGAGGGACACTTCTGTCTGTTTAAACAGACAGTCCATATCTGTGAGGCCACGCAATATTT	3129
Q	y	3118	TCTTAAACTCATGGGAGACAGCAGATTTCTGCCCTGTGTGAGGTCATTTGTCGCCATAT	3177
D	b	3130	TCTTAAACTCATGGGAGACAGCAGATTTCTGCCCTGTGTGAGGTCATTTGTCGCCATAT	3189
Q	y	3178	GTCTACCCCCCTGTCTTCATGAGGGAAAGTTGGAAATGGGGGCTACATATGCCCTCTCC	3237
D	b	3190	GTCTACCCCCCTGTCTTCATGAGGGAAAGTTGGAAATGGGGGCTACATATGCCCTCTCC	3249
Q	y	3238	TCCCGCTCAAGAGTTGGTTTTTCCATCTGATCTCTTCCACTCTGTCTGAGGGGAAGAA	3297
D	b	3250	TCCCGCTCTACAGAGTTGGTTTTTCCATCTGATCTCTTCCACTCTGTCTGAGGGGAAGAA	3309
Q	y	3298	GGGGGCTGTGTCTCAGGCAGATTTGTGAATTCCTGTTCATATCCCTCTCTATCCACCC	3357
D	b	3310	GGGGGCTGTGTCTCAGGCAGATTTGTGAATTCCTGTTCATATCCCTCTCTATCCACCC	3369
Q	y	3358	CTGCGCTGATAATATGTTAGCCCATACCCCAATAACTGCTATATTAGACACCCCCAGC	3417
D	b	3370	CTGCGCTGATAATATGTTAGCCCATACCCCAATAACTGCTATATTAGACACCCCCAGC	3429
Q	y	3418	CAGTTTCTGGGCTGCTCTCTTTGCTGCAATGTTTTTACAGAGAAAGAAATTTCTTGCT	3477
D	b	3430	CAGTTTCTGGGCTGCTCTTTGCTGCAATGTTTTTACAGAGAAAGAAATTTCTTGCT	3489
Q	y	3478	ATTTTTTTTTTCAATAATTTACTATTTATGATGATTTAAAGTGTTTTATTAAGGACAGAGTT	3533

Db 3490 ATTATTTTTCATTAATTTACTATTATGATGATTAATTAAGTGTTTTTATTAAGGACAGATT 3549
QY 3538 CTCTTAGGGTGGGAGGGAATATTTGAGGAGGGCTGGGCTTTAGGGAAGGAATGGGA 3597
Db 3550 CTCTTAGGGTGGGAGGGAATATTTGAGGAGGGCTGGGCTTTAGGGAAGGAATGGGA 3609
QY 3598 AGCAACATTTTATTAAGTGTACTATTGCTTACTTTGCTTACTTTGATTTGTTAGGAATGGCA 3657
Db 3610 AGCAACATTTTATTAAGTGTACTATTGCTTACTTTGATTTGTTAGGAATGGCA 3669
QY 3658 ATCAATATATAAAGTGATATATGTTTAAATGTAATAAATTTAAATGAGTTATTTA 3713
Db 3670 ATCAATATATAAAGTGATATATGTTTAAATGTAATAAATTTAAATGAGTTATTTA 3725

RESULT 11
US-60-213-360-1871
; Sequence 1871, Application US/60213360
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymor
; TITLE OF INVENTION: Identified thereby
; FILE REFERENCE: GX-0014 P
; CURRENT APPLICATION NUMBER: US/60/213,360
; CURRENT FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 8347
; SOFTWARE: PERL Program
; SEQ ID NO 1871
; LENGTH: 3751
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 348086.4
US-60-213-360-1871

Query Match 98.3%; Score 3651.4; DB 65; Length 3751;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3710; Conservative 0; Mismatches 1; Indels 8; Gaps 5;

QY 1 ATTAACAGCCGCTGGTTAGGAAGGACGAGAGGGGGCTTCCTCTTTGGGACTTTTCA 60
Db 27 ATTAACAGCCGCTGGTTAGGAAGGACGAGAGGGGGCTTCCTCTTTGGGACTTTTCA 86
QY 61 TGCCTCGTTTTTTTTCAGATGTGGCTTGGCTTGGGGCGAAGGTCCACAGCCAGCTTA 120
Db 87 TGCCTCGTTTTTTTTCAGATGTGGCTTGGCTTGGGGCGAAGGTCCACAGCCAGCTTA 146
QY 121 AGCTTACTCTCTGTGAAAGGGGAAAGTATCCCTGTGGAAGCGGTAAACTTTGTGGAG 180
Db 147 AGCTTACTCTCTGTGAAAGGGGAAAGTATCCCTGTGGAAGCGGTAAACTTTGTGGAG 206
QY 181 GGGGTGGGACGAGTATCTTCCCATGCCAGCGAAGGTGTGGCTTTGAGCTGGTCC 240
Db 207 GGGGTGGGACGAGTATCTTCCCATGCCAGCGAAGGTGTGGCTTTGAGCTGGTCC 266
QY 241 AGGAGCGGCTCCAGCTGTCTGAGGGAGG--CCCGAGGGGGGGGGAGGTGGGCCACAGA 299
Db 267 AGGAGCGGCTCCAGCTGTCTGAGGGAGGCCCCGGAGGGGGGGGGAGGTGGGCCACAGA 326
QY 300 ACCGGGTTCTGTAAAGAGACGTTTGGGAAGATTTCGATTCCGAGAAGAGGAAGAACCGGAT 359
Db 327 ACCGGGTTCTGTAAAGAGACGTTTGGGAAGATTTCGATTCCGAGAAGAGGAAGAACCGGAT 386
QY 360 TGAAGAGAGCCAGCGGCTGAGGGGAGGGGGCTGCTAAGATGGCGTCCGCTCTCCG 419
Db 387 TGAAGAGAGCCAGCGGCTGAGGGGAGGGGGCTGCTAAGATGGCGTCCGCTCTCCG 446
QY 420 GGCCTGCTCTTCGGTGGTTTTTCATCTTTGATCCCGCGGTCCCTCTCTGTACCTTGT 479

Db 447 GGCCTGCTCTTCGGTGGTTTTTCATCTTTGATCCCGGGTCCCTCTCTGTACCTTGT 506
QY 480 CCT--CAGCATCTGGAATCAAGAGAGCCCAT--GGCATCTGAGGTGCTTTATGCTCTGGC 535
Db 507 CCTCAGCAGCATCTGGAATCAAGAGAGCCCATGGGCATCTGAGGTGCTTTATGCTCTGGC 566
QY 536 ATGCCCAT--CAAGAAATAGGCCATAGAGTGTGATTTCTCAGGAGAGCAACATATAA 594
Db 567 ATGCCCATCAAGAAATAGGCCATAGAGTGTGATTTCTCAGGAGAGCAACATATAA 626
QY 595 AAGACAACTCATCAGCCTTGAAGGTGCCATCCAGTTAGGATTAACCCACACTGTGGG 654
Db 627 AAGACAACTCATCAGCCTTGAAGGTGCCATCCAGTTAGGATTAACCCACACTGTGGG 686
QY 655 GAGCCTGAGTACCAACACAGAGCGTGTATCTCATGCAAGATTTCTACGTGGTTGAGAG 714
Db 687 GAGCCTGAGTACCAACACAGAGCGTGTATCTCATGCAAGATTTCTACGTGGTTGAGAG 746
QY 715 TATCTTTTCCAGTGAAGGAGCAACCTGACCCCTGCTCATCATTACATGACCTTTG 774
Db 747 TATCTTTTCCAGTGAAGGAGCAACCTGACCCCTGCTCATCATTACATGACCTTTG 806
QY 775 TTTCAAGACTATGACCTTGTGCTTCCGCTACTTCCGGAGCTATTTGGTATCCGGCC 834
Db 807 TTTCAAGACTATGACCTTGTGCTTCCGCTACTTCCGGAGCTATTTGGTATCCGGCC 866
QY 835 CGATGATTACTTTGTATTCCTCTGCAAGTGGCGCTGATTTGAATCTGTAGCTCTGGAGC 894
Db 867 CGATGATTACTTTGTATTCCTCTGCAAGTGGCGCTGATTTGAATCTGTAGCTCTGGAGC 926
QY 895 TAGTGGTTCCCTATTTCTATGTTGTCAGGAGCATGATGATTTATTAAGACAGTCCACAA 954
Db 927 TAGTGGTTCCCTATTTCTATGTTGTCAGGAGCATGATGATTTATTAAGACAGTCCACAA 986
QY 955 TAAAGAGGCGGAATTTCTCAGAGCTGCTTCCAGGATACTACATCACTCAACACAGAA 1014
Db 987 TAAAGAGGCGGAATTTCTCAGAGCTGCTTCCAGGATACTACATCACTCAACACAGAA 1046
QY 1015 CCCTCGGACTTTGCTGCTTAAATTTCTATGAGCTGTACTGTGTGAGGAGGTGGCAAGAA 1074
Db 1047 CCCTCGGACTTTGCTGCTTAAATTTCTATGAGCTGTACTGTGTGAGGAGGTGGCAAGAA 1106
QY 1075 CATTCGGATTGGTGATGAACAACTCTTTTACCAAGATCGGTAAAAATGCATATCAATA 1134
Db 1107 CATTCGGATTGGTGATGAACAACTCTTTTACCAAGATCGGTAAAAATGCATATCAATA 1166
QY 1135 TGACCTCAAGGCTCAACCTTCAAAACGGGGCTTCCAGAGAGCGAGAGAGCTCT 1194
Db 1167 TGACCTCAAGGCTCAACCTTCAAAACGGGGCTTCCAGAGAGCGAGAGAGCTCT 1226
QY 1195 TCCACATTTAAAGACCTAGACTTTCTTACAAGACATCCCTGTATGGTCTTTTGTGATGC 1254
Db 1227 TCCACATTTAAAGACCTAGACTTTCTTACAAGACATCCCTGTATGGTCTTTTGTGATGC 1286
QY 1255 TGACATGTAACAGCTCTCTGTAAAGACCCCTGACGCTGATGTTTGGTGTGTCAGAGCTT 1314
Db 1287 TGACATGTAACAGCTCTCTGTAAAGACCCCTGACGCTGATGTTTGGTGTGTCAGAGCTT 1346
QY 1315 CAAGATAATGGAATTACAGCTCTTGTGATGTCATCCATATATAGATCATGCACACAGAGA 1374
Db 1347 CAAGATAATGGAATTACAGCTCTTGTGATGTCATCCATATATAGATCATGCACACAGAGA 1406
QY 1375 GCCCTTAAAGCAGTGAACACAGTACTCAGTTGATATCTCGAAGACCGGCCCCCAAGGC 1434
Db 1407 GCCCTTAAAGCAGTGAACACAGTACTCAGTTGATATCTCGAAGACCGGCCCCCAAGGC 1466
QY 1435 TCTGTATTCCACAGCCATGGAATCCATCCAGGAGAGGCTCGACGGGGTGGTACCATGGA 1494
Db 1467 TCTGTATTCCACAGCCATGGAATCCATCCAGGAGAGGCTCGACGGGGTGGTACCATGGA 1526
QY 1495 GACTGATGACCATATGGGTGGCATCCCTCCCGGATAGTTAAGGGGAAAGGCTCTGCT 1554
Db 1527 GACTGATGACCATATGGGTGGCATCCCTCCCGGATAGTTAAGGGGAAAGGCTCTGCT 1586

1555 TTATATGGCATCATTTGACATTTCTACAGTCTTACAGGTTTGTAAAGATTGGAGCACTC 1614
1587 TTATATGGCATCATTTGACATTTCTACAGTCTTACAGGTTTGTAAAGATTGGAGCACTC 1646
1615 TTGGAAGCCCTCGTATCATGACGAGACATGCTCAGTGCATCGCCAGGCTTCTACGC 1674
1647 TTGGAAGCCCTCGTATCATGACGAGACATGCTCAGTGCATCGCCAGGCTTCTACGC 1706
1675 TGAACGGTTCACAGCGCTTCATGTGCAACACAGATATTTAAGAAGATTCCTTTGAAGCCTTC 1734
1707 TGAACGGTTCACAGCGCTTCATGTGCAACACAGATATTTAAGAAGATTCCTTTGAAGCCTTC 1766
1735 TCTTCCAAAAAGTTTCGGTCTGGCTCATCTTCTCTGGCGAGCAGGCTTCAGTGGCAA 1794
1767 TCTTCCAAAAAGTTTCGGTCTGGCTCATCTTCTCTGGCGAGCAGGCTTCAGTGGCAA 1826
1795 CTCCTGATTTACTTACCAGCCATCGGTCTCTGGGGAACACAAAGCACAAGTGCACACAA 1854
1827 CTCCTGATTTACTTACCAGCCATCGGTCTCTGGGGAACACAAAGTGCACACAA 1886
1855 GGCAGAGTGGAGCCAGCGCTTCACTTGGTGTCTGTGATGTTTATCCTCAGACTCCACC 1914
1887 GGCAGAGTGGAGCCAGCGCTTCACTTGGTGTCTGTGATGTTTATCCTCAGACTCCACC 1946
1915 TTTTGGGGAATCAGTCAGGCTCGCCTATTCTGACCCAGTTCCTCACCTCTAGTTGG 1974
1947 TTTTGGGGAATCAGTCAGGCTCGCCTATTCTGACCCAGTTCCTCACCTCTAGTTGG 2006
1975 AGAGACTTTGCAATGTAACTACAACTGCAACCTTGGGAAAGCTTGAAGTTGCAGAGTC 2034
2007 AGAGACTTTGCAATGTAACTACAACTGCAACCTTGGGAGCTTGAAGTTGCAGAGTC 2066
2035 AGATTCAACCATTAAGCGCAAGCCTCAGAGACCTGGAACAGATTCGCGCATCTCTG 2094
2067 AGATTCAACCATTAAGCGCAAGCCTCAGAGACCTGGAACAGATTCGCGCATCTCTG 2126
2095 TGATCCCAAGATGTCAGCCCTTGGCCAGCAATGCTGAAATTTCTTCTACTTGGTCACTCA 2154
2127 TGATCCCAAGATGTCAGCCCTTGGCCAGCAATGCTGAAATTTCTTCTACTTGGTCACTCA 2186
2155 AAAAAGGAGTGAATAGAGTGAAGGAGTGTCTCTCCATCTTCTTCTTCTGAAGAAGAAC 2214
2187 AAAAAGGAGTGAATAGAGTGAAGGAGTGTCTCTCCATCTTCTTCTTCTGAAGAAGAAC 2246
2215 CTTCTCTCTCTCTCTCTCTCTCATGATGGGCTTAGTGGCTCAGAGAGTTGAGGACCGCA 2274
2247 CTTCTCTCTCTCTCTCTCTCATGATGGGCTTAGTGGCTCAGAGAGTTGAGGACCGCA 2306
2275 GCATCCCTCCACTCCAGAGTTGGTGTAGCGATTTTCAACTGGCCAAACCTTTTGCTC 2334
2307 GCATCCCTCCACTCCAGAGTTGGTGTAGCGATTTTCAACTGGCCAAACCTTTTGCTC 2366
2335 CACTATTGAATTTTTTTTTCAGACCCCACTTCTCATGCTGGAATGGGATGCTGGACTTG 2394
2367 CACTATTGAATTTTTTTTTCAGACCCCACTTCTCATGCTGGAATGGGATGCTGGACTTG 2426
2395 GCAGCTTCTTTTCCCTCGTCTTTGACTAGGACCGGACTCTTAATTTCTCAGACAGA 2454
2427 GCAGCTTCTTTTCCCTCGTCTTTGACTAGGACCGGACTCTTAATTTCTCAGACAGA 2486
2455 CTAGCTGACATATTCCTTACCTTAGTTCTTCTCTCTGACTCCTCGGAAGATCTCCT 2514
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2515 GTAATCTCTGAAGGTTTTTGGGGGATAAGGTTGTTTAAACCTCCAGCTTCTCTCT 2574
2547 GTAATCTCTGAAGGTTTTTGGGGGATAAGGTTGTTTAAACCTCCAGCTTCTCTCT 2606
2575 TCTTTTTTTTTTCTGAAAAAGGAAAAAGCACACAGCACAAATTTCAAGCATTTTCAG 2634
2607 TCTTTTTTTTTTCTGAAAAAGGAAAAA--CACACAGCACAAATTTCAAGCATTTTCAG 2664

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2725 GGTGTTTATGAAGAGAGAGTAGTGTCTCTGCGCAGAGCAGCTCTCTTTTAAACTCC 2784
2755 TCTCTCTCTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGTAATC 2814
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2815 TTTATCCCTTTTGTAAACACGAGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTTAG 2874
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3355 ACCCTGCTTGTGATATATGTTAGCCCATACCCCAATACTGTCTATATTAGACACCCCC 3414
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3685 CAAATACAAATATAAAGTGTATATGTTTAAATGTAATAAATCTTTAATCAGTTATTTA 3743

1736 CTTCCAAAGTTTGGCTCTGCTCATCTTTCTCTGGCGAGCAGGCTCCAGTGGCAAC 1795
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1796 TCCTGCAATTAATACAGGCAATCGGCTCTCTGGGGAACACAAAGGACAAAGTGAACAAAG 1855
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2515 GTAATCTGTAAAGTTTGGGGATTAAGGGTGTAAACCACTCCAGCTTT---CT 2571
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Db TCAGATCAGAACTCAGAGAGTGTGACAGATGCTATTCGTAGAGTTCCCTCAGAGAG 2736
2691 CATTGGTGTATGAGAGAGAGTGTGATGCTCTGCCAGAGCAGCTCTCTTTAAA 2750
Db CATTGGTGTATGAGAGAGAGTGTGATGCTCTGCCAGAGCAGCTCTCTTTAAA 2796
2751 CTCCTCTCTCTGATGAAATTTCTTAAGGCTGAGGATGAGAGTGGGACATGGGT 2810
Db CTCCTCTCTCTGATGAAATTTCTTAAGGCTGAGGATGAGAGTGGGACATGGGT 2856

2811 AATCTTTATCCCTTTTGTAAACAGGAGGAGCCATGGCTGGAGATCATAGCCCTTC 2870
Db AATCTTTATCCCTTTTGTAAACAGGAGGAGCCATGGCTGGAGATCATAGCCCTTC 2916
2871 CTAGGAGAAATCCTGTTCTACCTCCAGGCTATAGTAATTAATTAATTTTGA 2930
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2931 TATATTTCTGTTTGTCTTCTAAATGTGAAGACTTACCAATCAATTTTGAATCTCC 2990
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2991 AGAGGAGATTTTGTCTCTCTCATCTTTTCAACAGTGTCTCTCTGAGCT 3050
Db AGAGGAGATTTTGTCTCTCTCATCTTTTCAACAGTGTCTCTCTGAGCT 3096
3051 AGGTTAAAGAGGAGACATCTCTCTCTTAAACAGACAGTCCATATCTGTGAGGCCAGC 3109
Db AGGTTAAAGAGGAGACATCTCTCTCTTAAACAGACAGTCCATATCTGTGAGGCCAGC 3156
3110 AATATTTTCTTAACTCATGGGAGACAGAGATTTCTTGCCTTGGTGAGGTCATTTGCTG 3169
Db AATATTTTCTTAACTCATGGGAGACAGAGATTTCTTGCCTTGGTGAGGTCATTTGCTG 3216
3170 TGCCATATCTCTACCCCTCTCTTATGAGGAGGTTGAAATGGGGCTTACATATG 3229
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Db CCTCTCTCTCCGCTCTACAGAGTGTGCTTTCATCTGATCTCTCCACTCTCTCAG 3336
3290 GGGAGAGAGGGGCTCTGATCTCAGGAGATTTGTAATTTCTCTCTCTCTCTCTCT 3349
Db GGGAGAGAGGGGCTCTGATCTCAGGAGATTTGTAATTTCTCTCTCTCTCTCTCT 3396
3350 ATCCCACTCTGCTTGAATATATTTAGCCCATACCCCAATAACTGTCTATATTAGACA 3409
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3530 ACAGATTTCTGTTAGGGTGGGAGGGAATATTTGAGGAGGCTGGGTCTTAGGGAAGG 3589
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3590 AATGGGAGGACATTTTATTAAGTGTACTATTTGCTCTCTCTCTCTCTCTCTCTCT 3649
Db AATGGGAGGACATTTTATTAAGTGTACTATTTGCTCTCTCTCTCTCTCTCTCTCT 3696
3637 AATGGGAGGACATTTTATTAAGTGTACTATTTGCTCTCTCTCTCTCTCTCTCTCT 3709
Db AATGGGAGGACATTTTATTAAGTGTACTATTTGCTCTCTCTCTCTCTCTCTCTCT 3756
3710 TTTA 3713
Db TTTA 3760

RESULT 13

US-60-212-356-49/c

; Sequence 49, Application US/60212356

; GENERAL INFORMATION:

; APPLICANT: Beasley, Ellen

; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE

; TITLE OF INVENTION: PROTEINS, AND USES THEREOF

FILE REFERENCE: CL000677
CURRENT APPLICATION NUMBER: US/60/212,356
CURRENT FILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 411
SOFTWARE: FaSTSeq for Windows Version 4.0
SEQ ID NO 49
LENGTH: 32768
TYPE: DNA
ORGANISM: HUMAN
US-60-212-356-49

Query Match 81.8%; Score 3038.4; DB 65; Length 32768;
Best Local Similarity 91.2%; Pred. No. 0;
Matches 3420; Conservative 0; Mismatches 276; Indels 56; Gaps 16;

QY 2 TTAAACAGCGCGTGTAGGAAGACGAGAGAGGCGGCTCGCTCCTTTGGGACTTTTCAT 61
DB 12171 TAAACAGCGCGTGTAGGAGGACGAGAGGCGGCTCGCTCCTTTGGGACTTTTCAC 12112

QY 62 GCCTCG-----TTTTTTTTCAGATGTGGCTTGGGCGCAAGGTCCAGAGGCC 114
DB 12111 GCCTCGTTTTTTTTTCTTCAGATGTGGCTTTTCTCGAGCGAGGTCCTCAAGCAGTC 12052

QY 115 AGCTTAAGCTTACTCTCTGTAAGGGAAGTATCCCTGTGGAAGCGGTTAAACTT 174
DB 12051 AGCTTAAGCTTACTCTCTGTAAGGGAAGTATCCCTGTGGAAGCGGTTAAACTT 11992

QY 175 GTGAGGCGGTGGGACGTGTAGTCTTCCCATGTCAGGCGGAATGGTGTGGCTTTGAGC 234
DB 11991 GTGAGGCGGTGGGACGTGTAGTCTTCCCATGTCAGGCGGAATGGTGTGGCTTTGAGC 11932

QY 235 TGTTCAGAGCGCGGTC---GACGTGTCTGAGGAGG-CCCGAGGGGCGGGGAGGTG 290
DB 11931 TGTTCAGAGCGCGGTCGATGACAGGTCTGAGGAGGCGCCAGAGCGCGGAGGTG 11872

QY 291 GCCCAGAGACGCGGTTCTGTAAAGAGAGCTTGGGAGAGTTCGATTCGAGAGAGGAA 350
DB 11871 GCCCAGAGACGCGGTTCTGTAAAGAGAGCTTGGGAGAGTTCGATTCGAGAGAGGAA 11812

QY 351 GAACCGGATTGAAGAGAGCGAGCGGCTCAGGAGGAGGGGCTGTAAAGTGGCGTCGG 410
DB 11811 GAGCGGATGGAAGAGAGCGAGCGGCTCAGGAGAGGGGCTGCCAGATGGCGTCGG 11752

QY 411 CTTCTCCGCGCGCTGTCTTCGCTCGGTTTTTCATCTTTTGTATCCCGCGTCCCTTCCT 470
DB 11751 CTTCTCCCAACCGTGTGCGGCTCGGTTTTTCATCTTTGTATCCCGGCGCTTCCT 11692

QY 471 GTACCTTGCTCAGCATCTGGATCAAGAGACCCATGGCATCTGAGGTGCTTATGCTCT 530
DB 11691 GTACCGGCTCTCAGCATCTGGATCTTGAGCCCAAGCATCTGAGGTGCTTATGCTCT 11632

QY 531 CTGGCATGCCCCATCAAGAAATAGGCCATAGAAGTGTGATTTCTCAGGAGAGACAACAT 590
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QY 591 ATAAAAGACAACCTCATAGCCTTGAAGGTCGCAATCCAGTTAGGCAATTTACCCACATG 650
DB 11571 ATAAAAGACAACCTCAACAGCCTTGAAGGTCGCAATCCAGTTAGGCAATTTACATCTG 11512

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DB 11391 TTGGTTTCAAGACCTATGACCTGTGCTCTTCGCTACTTTCCGGAGCTATTTGGTATCC 11332

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DB 11331 GGCCCGATGATTAATTTGATTTCCCTCTGCAAGTGGAGCGGCTGATGAACTCTGTAGCTCTG 11272

DB 11331 CGCCCGATGATTAATTTGATTTCCCTCTGCAAGTGGAGCGGCTGATGAACTCTGTAGCTCTG 11272

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DB 11271 GAGCTAGTGTGTTCCCTTATTTCTATGTCTCCAGCGACGATGAACTCAATTTATTAAGACAGTCC 11212

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QY 1131 AATATGACCTCAAGGCTCAACCTCAAAACGCGGGCTTCCAGAAAGAGCGAGAGAAC 1190
DB 11031 AATATGACCTCAAGGCTCAACCTCAAAACGCGGGCTTCCAGAAAGAGCGAGAGAAC 10972

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DB 10731 AAAAGGCTCTGATTTCCACAGCCATGGAATTCATCAGGAGAGAGGCTCGGCTGGCGACA 10672

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DB 10671 CCATGAGGCGGATGACCATATAGGTGGCATCTCTGTCAGAAATAGTAAAGGGAAGAGGC 10612

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DB 10611 TTCTGCTTTTATATTGGCATCATTTGACATTTACAGTCTTACAGGTTGTGTAAGAGTTGG 10552

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DB 10551 AGCACTCTTGGAAAGCCCTGGTACATGAGGAGACACTGTCTCAGTGCATCGGCCAGGCT 10492

QY 1668 TCTACGCTGAACGGTTCCAGCGCTTCAATGTGCAACAGTATTTAAAGAAATTTCCCTTGA 1727
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QY 1728 AGCCTTCTCTCTCCAAAAGTTTCGGTCTGGCTCATCTTCTCTCGCGGAGAGGCTCCA 1787
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QY 1788 GTGGCAACTCTCTCATTTACTTACAGCCATCGGTCTCTGGGGAACAACAGGCAACAGTGA 1847
DB 10371 GTGGCAACTCTCTCATTTACTTACAGCCATTTGGTCTCTGGGGAACAACAGTCAACAGTG- 10313

QY 1848 CAACAAAGGCGAAGTGGAGCCAGCGGCTTCACTTGGTGTCTGCTGATGTTTACCTCAGA 1907
DB 10312 --ATAAGGTGCAAGTGGAGCCAGGTTTCACTTGGTGTCTGATGTTTACCTCAGA 10255

QY 1908 C-----TCCACCTTTGGAGGAAATCAGTGGAGGCTCGCTATTTCTGACCCAGTTTC 1960
DB 10254 CTTCAAGATTCACCTTTGGAGGAAATCAGTGGAGGCTC-ACTATTACTGACCAAGTTTC 10196

Db 12172 TAAACAGCCGTTGGTAAAGGAGGACAGAGAGCGCGCGTTTCCTCTCGGACCTTTTCAC 12113
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Db 12112 GCCTCGTTTTTGTGTTTTTCTTCAGATGTGGCTTTTCTTCAGCGAGGGTCCAGCAGTC 12053
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Qy 175 GTGAGGGGGTGGGAGCGTGAAGTCTTCCCATGCCAGCGAATGTGTGGCTTCGAGC 234
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Qy 235 TGGTCCAGGAGCGGCTC---GAGCTGTCTGAGGAGG-CCCGAGGGGCGGGGAGGTG 290
Db 11932 TGGTCCAGGAGCGGCTCGATGACAGGTCTGAGGAGGCGCCAGAGCGCGGGAAGTG 11873
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Qy 951 AACATAAGAGGGGGAATTTCTGCAGAGCTGCTTCCAGGATACATCAACTCAACC 1010
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Db 10552 AGCACTCTTGGAAAGCCCTGTTACATGAGCGGACACTGTCTCAGTGCACTCGCCAGGCT 10493
Qy 1668 TCTACGCTGAACGGTTCCAGCGCTTCATGTGCAACACAGTATTTAAAGAGATTTCCCTTGA 1727
Db 10492 TCTACGCTGAACGGTTCCAGCACTTCATGTGCAACGAGTATTTAAAGAGATTTCCCTTGA 10433
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Title: US-10-003-354-3

Perfect score: 3713

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 783854 seqs, 621352466 residues

Total number of hits satisfying chosen parameters: 1567708

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- Database : Published Applications NA.*
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 - 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	551.4	14.9	553	10	US-09-998-598-1241 Sequence 1241, Ap
2	469.8	12.7	598	10	US-09-864-761-13058 Sequence 13058, A
3	408	11.0	1899	10	US-09-954-456-827 Sequence 827, App
C 4	356.2	9.6	451	9	US-09-292-758-55 Sequence 55, Appl
5	312.2	8.4	398	9	US-09-918-995-3253 Sequence 3253, Ap
6	285	7.7	346	10	US-09-864-761-29620 Sequence 29620, A
7	152	4.1	350	10	US-09-783-590-9100 Sequence 9100, Ap
8	102.8	2.8	497	9	US-09-918-995-5650 Sequence 5650, Ap
9	75	2.0	2580	9	US-09-938-842A-2662 Sequence 2662, Ap
10	73.8	2.0	1266	9	US-10-012-055-3 Sequence 3, Appli
11	73.8	2.0	3224	9	US-10-012-055-1 Sequence 1, Appli
12	54.2	1.5	422	10	US-09-878-574-3267 Sequence 3267, Ap
13	52.6	1.4	337	10	US-09-878-574-3268 Sequence 3268, Ap
14	45.6	1.2	1837	10	US-09-833-381-1934 Sequence 1934, Ap
15	44.8	1.2	671	9	US-10-184-644-346 Sequence 346, App
16	44.8	1.2	671	9	US-10-184-634-346 Sequence 346, App
17	44	1.2	5979	9	US-10-239-676-18 Sequence 18, Appl
18	43.6	1.2	11812	9	US-10-239-676-18 Sequence 210, App
19	42.4	1.1	345	10	US-09-783-590-2746 Sequence 2746, Ap

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C	24	40.8	1.1	457	9	US-09-918-995-15437	Sequence 15437, A
	25	40.4	1.1	468	9	US-09-918-995-3720	Sequence 3720, Ap
	26	40	1.1	594	9	US-10-123-155-10	Sequence 10, Appl
	27	39.8	1.1	15732	9	US-10-239-676-95	Sequence 95, Appl
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	33	38.8	1.0	6478	9	US-10-239-676-124	Sequence 124, App
	34	38.8	1.0	7823	9	US-10-239-676-197	Sequence 197, App
	35	38.6	1.0	659158	9	US-09-771-208-20	Sequence 20, Appl
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C	37	38.2	1.0	465	9	US-09-918-995-26264	Sequence 26264, A
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	39	38.2	1.0	6282	9	US-10-239-676-127	Sequence 127, App
	40	38.2	1.0	7148	9	US-10-239-676-7	Sequence 7, Appli
	41	38.2	1.0	9539	9	US-10-239-676-52	Sequence 52, Appl
	42	38.2	1.0	139257	9	US-09-920-671-11	Sequence 11, Appl
C	43	38.2	1.0	640681	10	US-09-790-988-1	Sequence 1, Appli
	44	38	1.0	5127	9	US-10-239-676-131	Sequence 131, App
	45	37.8	1.0	4500	10	US-09-771-003-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-998-598-1241/c
; Sequence 1241, Application US/09998598
; Patent No. US20020150922A1
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Meagher, Madelein Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.561
; CURRENT APPLICATION NUMBER: US/09/998,598
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 2606
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 1241
; LENGTH: 553
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-998-598-1241

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; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
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; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 827
; LENGTH: 1899
; TYPE: DNA
; ORGANISM: Homo sapiens
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Matches 605; Conservative    0; Mismatches 280; Indels    9; Gaps    2;

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; Sequence 9100, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillion, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16-2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9100

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RESULT 8

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; Sequence 5650, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20

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; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5650
; LENGTH: 497
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
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US-09-918-995-5650

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Matches 182; Conservative 0; Mismatches 92; Indels 4; Gaps 2;

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US-09-938-842A-2662
; Sequence 2662, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME, AND METHODS OF USE
; FILE REFERENCE: SRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2662
; LENGTH: 2580
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2662

Query Match 2.0%; Score 75; DB 9; Length 2580;
Best Local Similarity 49.2%; Pred. No. 5.3e-11;
Matches 325; Conservative 0; Mismatches 315; Indels 21; Gaps 4;

QY 716 ATCTTCTTTTCCAGTGAAGGGAGCAACTGACCCCTGCTCATCACTACATGACTTTTCTG 775
DB 1426 ATGTTCTTCCCTAGAGCGGCTCCAAATTTTACCCCTCCACACAATCTGCGACTTCTCC 1485
QY 776 TTCAAGACCTATGCACTGTTGCGCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGCGCC 835

DB 1486 TCGAAGAGACTATTTGTCCTCATGGTTTTTCAGGAATTTTAAGGCAGATGTTCAAGTTAGATGCT 1545
QY 836 GATGATTACTTTGATTTCCCTCTGCACTGAGCCG---CTGATTGAACCTCTGTAGCTCTGGA 892
DB 1546 GCAGAGTACATGATGCTATTTTGTGTGTATGATGGCTGACAGAAATTTCTTCCCGGG 1605
QY 893 GCTAGTGGTTCCCTTATTTCTATGTCAGGAGATGATGTTCAATTAATTAAGACAGTCCAA 952
DB 1606 AAAAGTGGCAGTATCTTCTACCTTTCTCATGACGACAGATTTGTGTATCAAGACTTTAAAA 1665
QY 953 CATAAAGAGCGGGAATTTCTGCAAGAGCTGTTCCAGGATATCTACATGAACCTCAACCCAG 1012
DB 1666 AAGTCTGAGTTGAGGTTCTACTCAGAAATTTGCTTAAGTACTATGAACATGTAGGGAC 1725
QY 1013 AACCTCGGACTTTGCTGCTAAATTTCTATGACTGTACTGTGT---GCAGGCGAGTGGC 1069
DB 1726 CATGAAAAACACACTTATAACCAATTTTGTGGAGTTTCAAGAAATAACCTCAAGTGGGT 1785
QY 1070 AAGAACATTCGGATTTGCTGATGAACATCTTTTACCAGATCGGTAAATATGCATATC 1129
DB 1786 AAAAGGTACGCTTTGTAGTCTATGGGAATATGTTTGCACAGAAATTGAAGATTCATCGT 1845
QY 1130 AAATATGACCTCAAGGCTCAACCTACAAACGCGGGCTTCCAGAAAGAGCGAGAGAAG 1189
DB 1846 CGTTATGATCTAAAGGTTCAAC---TCAAGGAGATTTACTGAAAAGATCAAAATCCAA 1902
QY 1190 CTTCTTCCACATTTAAAGACCTAGACTCTTTTCAAGACATCCCTGATGCTCTTTTTTIG 1249
DB 1903 GAGAAGACCACTTGAAGATCT-----TGATCTAGCTTATGAATTTTCATATG 1950
QY 1250 GATGCTGACATGTACAAACGCTCTCTGTAAGACCCCTGACGCTGACTGTTTGGTCTGCAG 1309
DB 1951 GACAAGCTGTTACGGGAAGCCCTTTTCAAGCAAAATTTACTTAGACTGCTGTTTTGGA 2010
QY 1310 AGCTTCAAGATAATGGATTACAGCCTCTTGTATGTCATCAATATATAGATCATGCACAA 1369
DB 2011 TCGCTGAACATCATTCAGTCTTCTTACTGGGATTACATTTTAGAGCTCTCGGCCAA 2070
QY 1370 C 1370
DB 2071 C 2071

RESULT 10

US-10-012-055-3
; Sequence 3, Application US/10012055
; Patent No. US20020164750A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: 56634, A NOVEL HUMAN PHOSPHATIDYLINOSITOL 4-PHOSPHATE 5-KINASE
; FILE REFERENCE: 10448-114001
; CURRENT APPLICATION NUMBER: US/10/012,055
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/248,325
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1266
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-055-3

Query Match 2.0%; Score 73.8; DB 9; Length 1266;
Best Local Similarity 48.8%; Pred. No. 7e-11;
Matches 297; Conservative 0; Mismatches 297; Indels 15; Gaps 3;

QY 756 ATCACTACATGACTTTTCGTTTCAAGACCTATGCACTTGTGCTTCGCTTCCGCTACTTCGGG 815
DB 278 ATCTGCCAGTCAATTTCAAGTTCAGGAGTATTTGTCCTCCAGGCTTTTCAGGAACCTCCGTG 337

QY 816 AGCTATTGTTGTTATCCGCGCGATGATTTACTTGTATTCCTCTCGAGTGAGCGCGTGTATG 875
DB 338 ATCGATTGTCATTTGATGACCAAGATTTACTTGGTGTCCCTTACCCGAAACCCCGCCAGCG 397
QY 876 AACTCTGTAGCTCTGGAGCTAGTGGTTCCTTATTTCTATGTTGTCAGCGAGATGAGTTCA 935
DB 398 AAG-----TGAAGGCGAGTGGTGTCTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 448
QY 936 TTATTAAAGCAGTCCCAACATAAAGAGCGGAATTTCTGCAAGAGCTGCTTCCAGGATPACT 995
DB 449 TCATCAAGAGATGATCCAGTGAGGACATTGCTGACATGTCATAGCACTCTCCAACTATC 508
QY 996 ACATGAACCTCAACCAAGAACCTCG---GACTTTGCTGCTTAAATTTCTATGAGTGTACT 1052
DB 509 ACCAGTACATTTGTGAAGTGCATGCGCAACACGCTTCTGCCCCAGTTCTCTGGGATGTACC 568
QY 1053 GTGTGCGAGGCGGCAAGCAATTCGGATTGTTGGTGTGAACAATCTTTTACCAAGAT 1112
DB 569 GAGTCAGTGTGGACCAAGACAGTACATGCTTGTGTGCGCAATATGTTTAGCCACC 628
QY 1113 CGGTAAAAATGTCATATCAAAATATGACCTCAAGGCTCAACCTCAACACGCGCGCTTCCC 1172
DB 629 GTCTTCTGTGACAGGAGTATGACCTCAAGGCTTCCCTAGTGTCCGCGGAGCCAGCG 688
QY 1173 AGAAGAGCGAGAGAACCTTCCCAATTTAAAGACCTAGAGCTTCTTACAAGACATCC 1232
DB 689 ATAAGGAAAAGTTAAAGATTTGCCACCTTAAAGATATGAGCTTCTCTCAACAAAGAAC 748
QY 1233 CTGATGCTCTTTTGTGATGCTGACATGATGACAGCTCTCTGTAAGACCTCGAGCGTG 1292
DB 749 AGAAGATATATTTGTTGAAGAGGAGAAATATTTTCG---AGAAGCTGAAGAGAG 805
QY 1293 ACTGTTTGTGCTGACAGCTTCAAGATATGATTAAGCTCTCTGTAAGACCTCGAGCGTG 1352
DB 806 ATGTGGAGTTCTAGTGACGCTGAGATCATGACTACAGCTTCTGCTAGGATCCAG 865
QY 1353 ATATAGATC 1361
DB 866 ACATCATTC 874

RESULT 11

US-10-012-055-1
; Sequence 1, Application US/10012055
; Patent No. US20020164750A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: 56634, A NOVEL HUMAN PHOSPHATIDYLINOSITOL 4-PHOSPHATE 5-KINASE
; FILE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-114001
; CURRENT APPLICATION NUMBER: US/10/012,055
; CURRENT FILING DATE: 2001-11-13
; PRIOR FILING DATE: 2001-11-13
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3224
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (73) ... (1335)
US-10-012-055-1

Query Match 2.0%; Score 73.8; DB 9; Length 3224;
Best Local Similarity 48.8%; Pred. No. 1.4e-10;
Matches 297; Conservative 0; Mismatches 297; Indels 15; Gaps 3;

QY 756 ATCACTACATGACTTTCGTTTCAAGACCTATGCACTGTTCGCTTCCGCTACTTCGGG 815
DB 756 ATCACTACATGACTTTCGTTTCAAGACCTATGCACTGTTCGCTTCCGCTACTTCGGG 815

DB 350 ATCTGCCAGTCATTTCAAGGATTTATGTTCCCGAGGTTCTTCAGGAACCTCGTG 409
QY 816 AGCTATTGTTGATTCGCGCGCGATGATTTACTTGTATTCCTCTCGAGTGAGCGCGTGTATG 875
DB 410 ATCGATTGTCATTTGATGACCAAGATTTACTTGGTGTCCCTTACCCGAAACCCCGCCAGCG 469
QY 876 AACTCTGTAGCTCTGGAGCTAGTGGTTCCTTATTTCTATGTTGTCAGCGAGATGAGTTCA 935
DB 470 AAG-----TGAAGGCGAGTGGTGTCTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 520
QY 936 TTATTAAAGCAGTCCCAACATAAAGAGCGGAATTTCTGCAAGAGCTGCTTCCAGGATPACT 995
DB 521 TCATCAAGAGATGATCCAGTGAGGACATTGCTGACATGTCATAGCACTCTCCAACTATC 580
QY 996 ACATGAACCTCAACCAAGAACCTCG---GACTTTGCTGCTTAAATTTCTATGAGTGTACT 1052
DB 581 ACCAGTACATTTGTGAAGTGCATGCGCAACACGCTTCTGCCCCAGTTCTCTGGGATGTACC 640
QY 1053 GTGTGCGAGGCGGCAAGACATTCGGATTGTTGGTGTGAACAATCTTTTACCAAGAT 1112
DB 641 GAGTCAGTGTGGACCAAGACAGCTACATGCTTGTGTGCGCAATATGTTTAGCCACC 700
QY 1113 CGGTAAAAATGTCATATCAAAATATGACCTCAAGGCTCAACCTCAACACGCGCGCTTCCC 1172
DB 701 GTCTTCTGTGACAGGAGTATGACCTCAAGGTTCCCTAGTGTCCGCGGAGCCAGCG 760
QY 1173 AGAAGAGCGAGAGAACCTTCTCCACATTTAAAGACCTAGAGCTTCTTACAAGACATCC 1232
DB 761 ATAAGGAAAAGTTAAAGATTTGCCACCTTAAAGATATGAGCTTCTCTCAACAAAGAAC 820
QY 1233 CTGATGCTCTTTTGTGATGCTGACATGATGACCTCAAGGTTCCCTAGTGTCCGCGGAGCCAGCG 1292
DB 821 AGAAGATATATTTGTTGAAGAGGAGAAATATTTTCG---AGAAGCTGAAGAGAG 877
QY 1293 ACTGTTTGTGCTGACAGCTTCAAGATATGATTAAGCTCTCTGTAAGACCTCGAGCGTG 1352
DB 878 ATGTGGAGTTCTAGTGACGCTGAGATCATGACTACAGCTTCTGCTAGGATCCAG 937
QY 1353 ATATAGATC 1361
DB 938 ACATCATTC 946

RESULT 12

US-09-878-574-3267
; Sequence 3267, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 3267
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-013-Q1-B1-E8
US-09-878-574-3267

Query Match 1.5%; Score 54.2; DB 10; Length 422;
Best Local Similarity 52.4%; Pred. No. 2.2e-05;
Matches 144; Conservative 0; Mismatches 128; Indels 3; Gaps 1;

QY 722 TTTCCTCAAGTGAAGGAGCACTGACCCCTGCTCATCACTACATGACTTTCGTTCAAG 781
DB 722 TTTCCTCAAGTGAAGGAGCACTGACCCCTGCTCATCACTACATGACTTTCGTTCAAG 781

782 ACCTATGCACCTGTTGCTTCGGCTACTTCGGGAGCTATTGCTATCCGGCCCGATGAT 841
Db 112 GATTATGTCCTCCATGGTGTAAAGAAATTTGAAAACTGGTCAAGATTGATGCTGCCGAT 171
Qy 842 TACTGTATTCCTCTCT---CGAGTGAGCGCTGATTTGAACCTCTCTAGCTCTGGAGCTAGT 898
Db 172 TACATGATGTCATTTGTTGGAACGATACCTCTGAGGGAACCTATCTTCTCCGGGAAAAGT 231
Qy 899 GGTTCCTTATTCATGTCCTCAGGAGCATGATGATGTTCAATTAAGACAGTCCACATAAA 958
Db 232 GGTAGTGTCTTCTCTCTCTCAAGATGATGCTTTTCATGATCAAGACACTCCGGAAGATT 291
Qy 959 GAGCGGAATTTCTGCAGAACCTCTCCAGGATA 993
Db 292 GAATCAAGTCCCTTCAAGATGCTTCCAGACTA 326

RESULT 13
US-09-878-574-3268
; Sequence 3268, Application US/09878574
; Patent No. US200201105481
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878, 574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 3268
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-013-Q1-B1-E9
US-09-878-574-3268

Query Match 1.4%; Score 52.6; DB 10; Length 337;
Best Local Similarity 52.0%; Pred. No. 5.6e-05;
Matches 143; Conservative 0; Mismatches 129; Indels 3; Gaps 1;

Qy 722 TTTCCTCAGTGAAGGAGCAACCTGACCCCTGCTCATCACTACATGACTTTGTTTCAAG 781
Db 52 TTTCCTAAGAGAGTTCTCAATTAACACCTACTCATGAGTCAGATGATTTTAAATGAAA 111
Qy 782 ACCTATGCACCTGTTGCTTCCTGCTACTTCGGGAGCTATTGCTATCCGGCCCGATGAT 841
Db 112 GATTATGTCCTCATGGTGTAAAGAAATTTGAGAGAGCTGTTCAAGATTGATGCTGCCGAT 171
Qy 842 TACTGTATTCCTCTCAGT---GAGCGGTGATGAACTCTGCTAGCTCTGGAGCTAGT 898
Db 172 TACATGATGTCATTTGTTGGAACGATACCTCTGAGGGAACCTATCTTCTCCGGGAAAAGT 231
Qy 899 GGTTCCTTATTCATGTCCTCAGGAGCATGATGATTTCAATTAAGACAGTCCACATAAA 958
Db 232 GGTAGTGTCTTCTCTCTCTCAGGATGATGCTTTTCATGATCAATATTTGCGAAGATCT 291
Qy 959 GAGCGGAATTTCTGCAGAACCTCTCCAGGATA 993
Db 292 GAATCAAGTCCCTTCTTATTAATGCTTCCAGACTA 326

RESULT 14
US-09-833-381-1934
; Sequence 1934, Application US/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. US20020132090A1e1 Nucleic Acid and Protein Homologs

FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1934
; LENGTH: 1837
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: (1)---(1837)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1934

Query Match 1.2%; Score 45.6; DB 10; Length 1837;
Best Local Similarity 50.4%; Pred. No. 0.025;
Matches 139; Conservative 0; Mismatches 134; Indels 3; Gaps 1;

Qy 1086 TGGTATGAACTATCTTTTACCAAGATCGGTAAATGCAATATCAAAATATGACCTCAAAG 1145
Db 4 TTGTGATGCGCAATATGTTTAGCCACCGTCTTCTGTGCACAGGAAGTATGACCTCAAGG 63
Qy 1146 GCTCAACCTACAAACCGCGGCTTCCACAGAGCGAGAGAGCCCTTCCACATTTA 1205
Db 64 GTTCCCTAGTGTCCCGGAAGCCAGGATAGGAAGTTAAAGATTTGCCCCCTTA 123
Qy 1206 AAGACCTAGACTTTTACAGACATCCCTGATGGTCTTTTGGATGCTGACATGTACA 1265
Db 124 AGGATATGACCTTTCTCAACAAGAACCCAGAAAGTATATATTGTTGAAGAGGAGAAAAA 183
Qy 1266 AGCTCTCTGTAAGACCTTCGAGCGTACTGTTTGGTGTGCGAGCTTCAAGATTAATGG 1325
Db 184 TATTTCTGG---AGAGCTTGAAGAGAGATGTGGAGTTTCTAGTGCAAGCTCAAGATCATGG 240
Qy 1326 ATTACAGCTCTTGTATGTCAATCCATTAATATAGATC 1361
Db 241 ACTACAGCTTCTGTAGCAATCCAGCATCATTC 276

RESULT 15
US-10-184-644-346
; Sequence 346, Application US/10184644
; Publication No. US20030044930A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C227
; CURRENT APPLICATION NUMBER: US/10/184,644
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 346
; LENGTH: 671
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-644-346

Query Match 1.2%; Score 44.8; DB 9; Length 671;
Best Local Similarity 6.2%; Pred. No. 0.02;

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Matches 24; Conservative 150; Mismatches 215; Indels 0; Gaps 0;
Qy 132 CTGTGAAGGGGAAGTATCCCTGTGGAAGCGGTAAACTTGTGAGGGGTGCGGGA 191
   : : | : : : : : : : : : : : : | : : : : : : : :
Db 175 SDLQASVSPSEBESSEKTSQDFTPEKAAVRAPRGLGRKKKAPSADS 234
   : : : : : : : : : : : : : : : : : : : : : : : :
Qy 192 CGTGATCTTCCCATCCAGGCGAATGGTGTGCCTTGAGCTGGTCCAGGACCGGCT 251
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 235 DSKADSDGAKPEPVAMAKSASSSSSSSSSDSVKPPPRGRPAEKPLPKPRKPKP 294
   : : : : : : : : : : : : : : : : : : : : : : : :
Qy 252 CGAGTGTCTGAGGAGCGCGGAGGGGGGAGGTGGCCACAGAACCGGGTCTG 311
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 295 ERPFSSSSSDSDSDVDRISEWKRDEARRRELEARRRREBEELRLRLEKEKEKERR 354
   : : : : : : : : : : : : : : : : : : : : : : : :
Qy 312 TAAAGAGACGTTGGAGATTTCGATTCGAGAGAGGAAGAACCGGATTGAAAGAGAGCC 371
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 355 ERADRGAEARGSGGSDGLREDDEPVKRGKRGPPSSSDSEPEALELEREAKKSAAK 414
   : : : : : : : : : : : : : : : : : : : : : : : :
Qy 372 AGCGCGTGTAGGGGAGGGGCTCTAAGATGGCGTCCGCTCCTCCGGGCGGTCGCTT 431
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 415 KPQSSSTEPARKPGQKEKRVPEKQQAQPVKVERTRKRSEGFMDRKVKKKKPSVEEK 474
   : : : : : : : : : : : : : : : : : : : : : : : :
Qy 432 CGGTGCGGTTTTTTCATCTTTCATCCGCGGTCCTCTCTGTACCTTGTCTCAGCATCTG 491
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 475 LQKLHSEIKFALKVDSPDVKCLNABELGLQVTSQILQKNTDVTATLKIRRYKANKD 534
   : : : : : : : : : : : : : : : : : : : : : : : :
Qy 492 GAATCAAGAGACCATGGCATCTGAGGTG 520
   : : : : : : : : : : : : : : : : : : : : : : : :
Db 535 VMEKAAEVYTRLSRVLGPKEAVQKYNK 563
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Job time : 514 secs

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OM nucleic - nucleic search, using sw model

Run on: May 13, 2003, 00:45:33 ; Search time 185 Seconds
(without alignments)
6155.085 Million cell updates/sec

Title: US-10-003-354-3
Perfect score: 3713
Sequence: 1 attaacaggcgtggttagg.....aaacttaataagtgattatta 3713

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfilee1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55.4	1.5	7218	1	US-08-232-463-14
2	51.4	1.4	7218	1	US-08-232-463-14
3	42.6	1.1	7218	1	US-08-451-405A-2
4	38.2	1.0	87350	3	US-08-781-891-79
5	38.2	1.0	87543	4	US-09-791-211-3
6	37.8	1.0	1086	4	US-09-134-001C-1208
7	37.6	1.0	624	4	US-09-397-992A-3
8	36	1.0	624	4	US-09-397-992A-6
9	36	1.0	1983	4	US-09-453-702B-36
10	36	1.0	53526	3	US-08-658-136-2
11	36	1.0	53577	3	US-08-658-136-1
12	35.8	1.0	549	4	US-09-118-442-26
13	35.8	1.0	549	4	US-09-677-064-26
14	35.8	1.0	1164	4	US-09-134-001C-2534
15	35.8	1.0	1166	4	US-09-072-596-323
16	35.8	1.0	3095	6	5231168-1
17	35.8	1.0	19124	2	US-08-487-826B-13
18	35.6	1.0	26385	3	US-08-961-527-3
19	35.4	1.0	1590	3	US-08-747-221B-23
20	35.4	1.0	1590	4	US-09-005-051-23
21	35.4	1.0	1650	3	US-08-747-221B-21
22	35.4	1.0	1650	3	US-08-747-221B-22
23	35.4	1.0	1650	4	US-09-005-051-21
24	35.4	1.0	1650	4	US-09-005-051-22
25	35.4	1.0	1792	3	US-08-747-221B-18
26	35.4	1.0	1792	3	US-08-747-221B-20
27	35.4	1.0	1792	4	US-09-005-051-18

28	35.4	1.0	1792	4	US-09-005-051-20
29	35.4	1.0	2219	5	PCT-US93-07213-4
30	35.4	1.0	2870	5	PCT-US93-07213-3
31	35.4	1.0	3102	5	PCT-US93-07213-1
32	35	0.9	865	4	US-09-040-984-71
33	35	0.9	865	4	US-09-123-913-71
34	35	0.9	865	4	US-09-643-597-71
35	35	0.9	1969	1	US-08-356-340-1
36	35	0.9	1969	2	US-08-786-553-1
37	35	0.9	2566	2	US-08-488-940-19
38	34.6	0.9	35081	2	US-08-752-760A-1
39	34.4	0.9	1766	4	US-08-961-527-235
40	34.2	0.9	2659	3	US-08-749-522-1
41	34.2	0.9	2755	3	US-08-749-522-2
42	34.2	0.9	56516	2	US-08-996-306-1
43	34.2	0.9	56516	4	US-09-338-907-1
44	34.2	0.9	56516	4	US-09-218-207-1
45	34	0.9	421	4	US-08-642-274D-55

ALIGNMENTS

RESULT 1
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-9300
; TELEFAX: (703) 836-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZpmt-Fls
; US-08-232-463-14

Query Match 1.5%; Score 55.4; DB 1; Length 7218;

QY 3470 TTCTTGCTATTTTTTTTTCATATTTACTATTTATGATGATTTAAGTGTATTTAAGG 3529
Db 281 TTTTTTTTTTTTTTTGTGTTGTTGTTTCCAAATCCAAAAATATCTGAATTTTTTTTTTGA 222
QY 3530 ACAGAGTTCTGTTAGGGGTGGAGGGAATATTTGAGGGAGGGCTGCTTTAGGGAAGG 3589
Db 221 ATTTCTTATCATATACCGTCACAAATCTATTTTAGGTTCACTATGTTTAATATAATTT 162
QY 3590 AATGGGAAGCAACATTTTTTATTAAGTGTACTATTTGCTCTACTTTGATTTGTTTCA 3649
Db 161 TAAATACAAATAAAACCTCTTCAATAGAAATATTTTATCTAAATTTTTTATTTTTTAA 102
QY 3650 AATGGCAATACATATAAAAGTGATATGTTTAAATGTATAAACTTTAATGAGTTA 3709
Db 101 AAAATAAAATAAAATAAAATAAAAGGAAAAAAGAAAAAACAATACTAATCAATATTTATCA 42
QY 3710 T 3710
Db 41 T 41

RESULT 4

US-08-781-891-79
; Sequence 79, Application US/08/781891
; Patent No. 6090620
; GENERAL INFORMATION:
; APPLICANT: Fu, Ying-Hui
; APPLICANT: Yu, Chang-En
; APPLICANT: Oshima, Junko
; APPLICANT: Mulligan, John T.
; APPLICANT: Schellenberg, Gerald D.
; TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
; TITLE OF INVENTION: WERNER'S SYNDROME
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,891
; FILING DATE: 27-DEC-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6090620tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 240052.419
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87350 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-781-891-79

Query Match 1.0%; Score 38.2; DB 3; Length 87350;
Best Local Similarity 47.0%; Pred. No. 7.8;
Matches 118; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 3449 TTTTTCACAGAGGAAGATTTCTGCTATTTTTCATATTTTACTATTTATGATG 3508
Db 45681 TTTATAGTATGAAGAAATTAATCATACATAGTTTATTTATCTAATTTCTAAATACCCTG 45740

QY 3509 TATTTAAGTCTTTTATTAAGGACAGAGTTCTGTAGGGGTGGAGGGAATATTTGAGGGA 3568
Db 45741 GAAGAAAAATGAAATTTAATGGAATGTAGTTCTGTATTTACTTTGTTTCGAGTGTGGAAAAAT 45800
QY 3569 GGGCTGGTCTTAGGGGAAGGAATGGGGAAGCAACATTTTTTATTAAGTGTACTATTTGC 3628
Db 45801 TTATATGGTCTTTCTTAAACAGCAGCTGTCAGTAGAANAACAATGTGAGCTACATATGCAA 45860
QY 3629 CTCTACTTTTGTATTTGTTTCAAGAAATGCAAAATACAATAAAGTGATATATGTTTAAAT 3688
Db 45861 TTTTAAATTTCTAGTAGCCACATTTTAAAGTAATGATGCAATTTATTTTGTATAAT 45920
QY 3689 GTAATAAATCTT 3699
Db 45921 ATAATTTAAT 45931

RESULT 5

US-09-791-211-3
; Sequence 3, Application US/09791211
; Patent No. 6448080
; GENERAL INFORMATION:
; APPLICANT: Donna T. Watt
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF WRN EXPRESSION
; FILE REFERENCE: RTS-0205
; CURRENT APPLICATION NUMBER: US/09/791,211
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 3
; LENGTH: 87543
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 7421
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 7427
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 11609
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 12605
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 12742
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 29370
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 29422
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 29979
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 29980
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 29981
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 30136
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 30140
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 31205

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; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 31206
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 31592
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 33095
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 33160
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 34066
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 34072
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 36816
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 39020
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 42164
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 42459
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 46808
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 46823
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
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; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 47291
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 52786
; OTHER INFORMATION: unknown
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; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 53384
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 54684
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 59215
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 59235
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 59242
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 63290
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 66614
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 68660
; OTHER INFORMATION: unknown
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; NAME/KEY: unsure
; LOCATION: 68697
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 68718
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 68733
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 68739
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 69785
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 79134
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 79198
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 86336
; OTHER INFORMATION: unknown
; OTHER INFORMATION:
; US-09-791-211-3
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Query Match 1.0%; Score 38.2; DB 4; Length 87543;

Best Local Similarity 47.0%; Pred.No. 7.8; Indels 0; Gaps 0;
Matches 118; Conservative 0; Mismatches 133;

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QY 3449 TTTTTCACGAAGGAAGAAATCTTGCTATTATTTTTCATAATTTTACTATTTATGATG 3508
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 45874 TTTATAGTATGAAGAAATTAATCATACATAGTTTATTTATCTTAATTTCTAAATACCATG 45933
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3509 TATTTAAGTGTTTTATTAAGGACAGAGTTCTGTAGGGGTGGAGGGAATATTTGAGGGA 3568
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 45934 GAAGAAATGAATTTAATGGAATGTGTTACTTGTCTTCTGAGTGTGGGAAAT 45993
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3569 GGGCTGGTCTTAGGGAAGGAATGGGGAAGCAACATTTTATTAAGTCTTACTATTTCG 3628
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 45994 TTATATGGTCTTTCTTAAACAGACCTGTGAGTAGAAATACAATGTGAGCTACATATGCA 46053
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3629 CTCTACTTTGTATTGTTTCAGAAATGCAATACAAATATAAAAGTGATATATGTTTAAAT 3688
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 46054 TTTTAAATTTCTAGTAGCCACATTTTAAAGTAATGAATGATCAATTTATTTTGATAAT 46113
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3689 GTAATAAATCTT 3699
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 46114 ATAAATTAAT 46124
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 6

```
US-09-134-001C-1208
; Sequence 1208, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1208
; LENGTH: 1086
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; US-09-134-001C-1208
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Query Match          1.0%; Score 37.8; DB 4; Length 1086;
Best Local Similarity 55.8%; Pred. No. 0.51;
Matches 72; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 2916 TTTTGCATTTTGAATATATTTCTGTTCTTTTCTTAAATGGAAGACTTACCAATGAAT 2975
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 385 TATTTTCATATCATATATATGAGTCTTTTGTCTATCTTATATCATATTTACAAATTAAT 444

QY 2976 TTTAGATCATTTCTCGAGGAGATTTTTTTTTCCTCTCTCATCTTTTCCACAGTGTCT 3035
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 445 TTTAGATGTTTCAATAGTAAATTTTGTCTTTTGTCTTTAGCATTTATAGTCCAAATCTAT 504

QY 3036 CTTGTTTCT 3044
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 505 CTACATTAAT 513

RESULT 7
US-09-397-992A-3/c
; Sequence 3, Application US/09397992A
; Patent No. 6329175
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell
; APPLICANT: Grant, Francis J.
; APPLICANT: Rixon, Mark W.
; APPLICANT: Kindsvogel, Wayne
; TITLE OF INVENTION: Interferon-epsilon
; FILE REFERENCE: 98-46
; CURRENT APPLICATION NUMBER: US/09/397,992A
; PRIOR FILING DATE: 1999-09-16
; PRIOR APPLICATION NUMBER: 60/101,012
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/118,578
; PRIOR FILING DATE: 1999-02-05
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This degenerate sequence encodes the amino acid
; NAME/KEY: variation
; LOCATION: (1)...(624)
; OTHER INFORMATION: n is any nucleotide
US-09-397-992A-3

Query Match          1.0%; Score 37.6; DB 4; Length 624;
Best Local Similarity 27.2%; Pred. No. 0.4;
Matches 72; Conservative 60; Mismatches 130; Indels 3; Gaps 1;

QY 3421 TTTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTATT 3480
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 310 TTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTATT 251

QY 3481 TTTTTCATATTTTACTATTTATGATGATTTTAAAGTGTGTTTATTAAGGACAGAGTTCTG 3540
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 250 TTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTATT 194

QY 3541 TTAGGGGTGGGAGGAATATTTAGGGGAGGCTGGGTCTTAGGGAAGGAATGGGAGC 3600
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 193 TTTGNGGNARNARRAARTTTTNCRTGNGGNARRCAATGTTGDTATNSWNRNGTYTGN 134

QY 3601 AACATTTTATTAAGTGTACTATTTGCTCTACTTTGTTGTTTACAGAAATGCAATA 3660
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 133 RYTRTTNARNARYTTNARNSWYTCYTRTNACYTCGKTCYGTGRAADATDATNARYT 74

QY 3661 CAATATAAAGTGTATATGTTT 3685
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 73 TNARTCNARNSWRAADATNGTNGT 49

RESULT 9
US-09-453-702B-36
; Sequence 36, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; APPLICANT: Burland, Valerie
; APPLICANT: Perna, Nicole T.
; APPLICANT: Plunkett, Guy
; APPLICANT: Welch, Rod
; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
```

```
Db 73 TNARTCNARNSWRAADATNGTNGT 49

RESULT 8
US-09-397-992A-6/c
; Sequence 6, Application US/09397992A
; Patent No. 6329175
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell
; APPLICANT: Grant, Francis J.
; APPLICANT: Rixon, Mark W.
; APPLICANT: Kindsvogel, Wayne
; TITLE OF INVENTION: Interferon-epsilon
; FILE REFERENCE: 98-46
; CURRENT APPLICATION NUMBER: US/09/397,992A
; CURRENT FILING DATE: 1999-09-16
; PRIOR APPLICATION NUMBER: 60/101,012
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/118,578
; PRIOR FILING DATE: 1999-02-05
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This degenerate sequence encodes the amino acid
; NAME/KEY: variation
; LOCATION: (1)...(624)
; OTHER INFORMATION: n is any nucleotide
US-09-397-992A-6

Query Match          1.0%; Score 36; DB 4; Length 624;
Best Local Similarity 26.8%; Pred. No. 1.2;
Matches 71; Conservative 60; Mismatches 131; Indels 3; Gaps 1;

QY 3421 TTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTATT 3480
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 310 TTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTATT 251

QY 3481 TTTTTCATATTTTACTATTTATGATGATTTTAAAGTGTGTTTATTAAGGACAGAGTTCTG 3540
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 250 TTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTATT 194

QY 3541 TTAGGGGTGGGAGGAATATTTAGGGGAGGCTGGGTCTTAGGGAAGGAATGGGAGC 3600
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 193 TTTGNGGNARNARRAARTTTTNCRTGNGGNARRCAATGTTGDTATNSWNRNGTYTGN 134

QY 3601 AACATTTTATTAAGTGTACTATTTGCTCTACTTTGTTGTTTACAGAAATGCAATA 3660
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 133 RYTRTTNARNARYTTNARNSWYTCYTRTNACYTCGKTCYGTGRAADATDATNARYT 74

QY 3661 CAATATAAAGTGTATATGTTT 3685
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 73 TNARTCNARNSWRAADATNGTNGT 49

RESULT 9
US-09-453-702B-36
; Sequence 36, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; APPLICANT: Burland, Valerie
; APPLICANT: Perna, Nicole T.
; APPLICANT: Plunkett, Guy
; APPLICANT: Welch, Rod
; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
```


Qy 1551 TGCTTTATATTGGCATCATTTGACATTTCTACAGTCTTACAGGTTTCTTAAGAAGTTGGAGC 1610

Db 213 TCCTATTCTTTGGGATATCGACATCTCTCAGGATTACAGTTTAAAGAAAGCGGGCCGAGC 272

;; PRIOR APPLICATION NUMBER: US 60/055,779
;; PRIOR FILING DATE: 1997-08-14
;; NUMBER OF SEQ ID NOS: 5674
;; SEQ ID NO 2534
;; LENGTH: 1164
;; TYPE: DNA
;; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2534

Query Match 1.0%; Score 35.8; DB 4; Length 1164;
Best Local Similarity 49.7%; Pred. No. 2.1;
Matches 91; Conservative 0; Mismatches 92; Indels 0; Gaps 0;
QY 957 AAGAGGGGGAATTTCTGAGAGAGCTGCTCCAGGATACATGAACCTCAACAGAAACC 1016
Db 759 AACATCAGTAATACTGCACCATCATTTTCTTACACTATTTCTTACTGTGACTGTTC 700
QY 1017 CTCGGACTTGTCTCCTAATTTCTATGAGTACTGTGTGAGGAGGAGGCGCAAGAAC 1076
Db 699 TTCATTTAAAGTGGTTTAACTCTGCCAAGTGTCTGAGAGTAAGTTGAGGTTTAAATACT 640
QY 1077 TTCGGATTGTGATGACATCAATCTTTTACCAAGATCGGTAAATGCATATCAATATG 1136
Db 639 TTCATCTGATTAAATATTCACCTTTTCACTTTGAACGGTAAATTTCTTGGGAAATATT 580
QY 1137 ACC 1139
Db 579 ACC 577

RESULT 15

US-09-072-596-323/c
; Sequence 323, Application US/09072596
; Patent No. 6458366
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonia
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Hendrickson, Ronald C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS
; NUMBER OF SEQUENCES: 350
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/072,596
; APPLICATION NUMBER: US/09/072,596
; FILING DATE: 05-MAY-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.417C9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 323:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1166 base pairs
; TYPE: nucleic acid

;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: Genomic DNA
US-09-072-596-323
Query Match 1.0%; Score 35.8; DB 4; Length 1166;
Best Local Similarity 29.1%; Pred. No. 2.1;
Matches 83; Conservative 54; Mismatches 148; Indels 0; Gaps 0;
QY 163 GCGGTTAAACTTGTGAGGGGTGCGGAGCGTGAGTTCTTCCCATGCCAGGCGAATGGT 222
Db 559 GAGGGGAANKMTGSKRGKAGADMGTSGRKATNGGTGCMAGNGKTCAGRYNGSGG 500
QY 223 GTGGCCTTGTAGCTGTCTCCAGGAGCCGCTCGACGTGTCTGAGGGAGGCCCGGAGGGGCG 282
Db 499 GNKCANAGGWACCGGANKGARTGRGAKMKGGAGGRRRCNCRGGTGTGNTGAGRCSCG 440
QY 283 GGGAGTGGCCACACAGACCGGGTTCTGTAAAGAGACGTTGGGAAGATTTCGATTCCGAG 342
Db 439 KKGGRATGACCGAGGRTWGSMTGTCGGGGGKNRAKTASTCCNNGRAKAGRASACCKMK 380
QY 343 AAGAGGAAGAACCGGATTGAAAGAGAGCCAGGCCGCTGAGGGGAGGGGCTGCTAAGAT 402
Db 379 SAKTTSMGKSSAGNGKKAAGGMCNAARWNCCTTSCCGGRTTTRRSAAACCSACATT 320
QY 403 GCGCTCGGCTCTCCCGGGCCGCTGCTTTCGGTCTGGTTCATC 447
Db 319 CCGGTTACCGGTATTGAAACCGNACCCTGTCAGRTTTRTYACC 275

Search completed: May 13, 2003, 02:16:52

Job time : 709 secs

Qy	61	TGCGCTGTTTTTTTTTTCAGATGAGGCTGTGCTGCGGCGAAGGTCCAGACGCAAGCTTA	120
Db	61	TGCGCTGTTTTTTTTTTCAGATGAGGCTGTGCTGCGGCGAAGGTCCAGACGCAAGCTTA	120
Qy	121	AGCTTACTCTTCTGTGTAAGAGGGAGAAAGTATCCCTGTGAAAGCGGTATTAACCTTGTGAG	180
Db	121	AGCTTACTCTTCTGTGTAAGAGGGAGAAAGTATCCCTGTGAAAGCGGTATTAACCTTGTGAG	180
Qy	181	GGGGTGGGGGACGTGAGTTTCTTCCCATGCGACGGGAATGCTGTGGCTTGAAGCTGGTCC	240
Db	181	GGGGTGGGGGACGTGAGTTTCTTCCCATGCGACGGGAATGCTGTGGCTTGAAGCTGGTCC	240
Qy	241	AGGAGCGGCGTCGACGCTGTGTGAGGGAGG-CCCGAGGGGGGCGGGGAGGTGGCCACAGA	299
Db	241	AGGAGCGGCGTCGACGCTGTGTGAGGGAGGCCCGGAGGGGGCGGGGAGGTGGCCACAGA	300
Qy	300	ACGCGGGTTCGTAAAGAGACGTTTGGGAAAGTTTCGATTCGAGAAAGAGAAAGAACCGGAT	359
Db	301	ACGCGGGTTCGTAAAGAGACGTTTGGGAAAGATTTCGATTCGAGAAAGAGAAAGAACCGGAT	360
Qy	360	TGAAAGAGAGCGAGGCGCGTGAAGGGGGAGGGGGCGTGAAGTGGCGGTGGCGCTCCG	419
Db	361	TGAAAGAGAGCGAGGCGCGTGAAGGGGGAGGGGGCGTGAAGTGGCGGTGGCGCTCCG	420
Qy	420	GGCGGTGCTTCGCTCGGTGGTATTCATCCCTTGATCCCGGCTCCCTCTGTACCTTGT	479
Db	421	GGCGGTGCTTCGCTCGGTGGTATTCATCCCTTGATCCCGGCTCCCTCTGTACCTTGT	480
Qy	480	CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCTTATGCTCTGTGCAATGC	539
Db	481	CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCTTATGCTCTGTGCAATGC	540
Qy	540	CCATCAAGAAAAATGAGCCATAGAGAGTGTGATTCCTCAGAGAGACAAATATATAAAAAA	599
Db	541	CCATCAAGAAAAATGAGCCATAGAGAGTGTGATTCCTCAGAGAGAGCAAAATATATAAAAAA	600
Qy	600	CAACCTCATGACCTTGAAGAGTGCATCCATGTTAGGCAATNCCACACTGTGGGAGCC	659
Db	601	CAACCTCATGACCTTGAAGAGTGCATCCATGTTAGGCAATNCCACACTGTGGGAGCC	660
Qy	660	TGAGTACCAAAACGAGACGAGTGTCTCATATGCAAAATTTTCAAGCTGTGTGAGAGTATCT	719
Db	661	TGAGTACCAAAACGAGACGAGTGTCTCATATGCAAAATTTTCAAGCTGTGTGAGAGTATCT	720
Qy	720	TCTTCCAGTGAAGGAGGACACTGACCCCTGCTCATCATCAATGAATGACTTGGTTC	779
Db	721	TCTTCCAGTGAAGGAGGACACTGACCCCTGCTCATCATCAATGAATGACTTGGTTC	780
Qy	780	AGACTATGACACTGTGCTTCCGCTGATCTTCCGGAGCTATTTGGTATCCGGCCCATG	839
Db	781	AGACTATGACACTGTGCTTCCGCTGATCTTCCGGAGCTATTTGGTATCCGGCCCATG	840
Qy	840	ATTACTTGTATTTCCCTCGACAGTGAAGCGGTGATTAACATCTGTAGCTCTGGAGCTAGTG	899
Db	841	ATTACTTGTATTTCCCTCGACAGTGAAGCGGTGATTAACATCTGTAGCTCTGGAGCTAGTG	900
Qy	900	GTTTCCATTTCTATGTGTCCAGGACGATGATTTATTAAGACGTCCAACTAAAG	959
Db	901	GTTTCCATTTCTATGTGTCCAGGACGATGATTTATTAAGACGTCCAACTAAAG	960
Qy	960	AGCGGGAATTTCTGACAGAGCTGTTCCAGAGATCAATGAACCTCAACGAAACCTCTC	1019
Db	961	AGCGGGAATTTCTGACAGAGCTGTTCCAGAGATCAATGAACCTCAACGAAACCTCTC	1020
Qy	1020	GGACTTTCCTGCTAAATTTCTATGACTGTATGCTGTGAGGCAAGGTGCAAGAACTTC	1079
Db	1021	GGACTTTCCTGCTAAATTTCTATGACTGTATGCTGTGAGGCAAGGTGCAAGAACTTC	1080
Qy	1080	GGAATTGTGTATGAACAATTTTATCAAGATTCGTTAAAAATGCAATATATATGAC	1139
Db	1081	GGAATTGTGTATGAACAATTTTATCAAGATTCGTTAAAAATGCAATATATATGAC	1140

Qy	1140	TCGAAGCTCAACCTCAACAAAGGGGGGCTTCCGAGAAAGACGAGAGAAGGCTCTCCCA	1199
Db	1141	TCAAAGGCTCAACCTCAACAAAGGGGGGCTTCCGAGAAAGACGAGAGAAGGCTCTCCCA	1200
Qy	1200	CATTTAAGAAGCTTAGACTCTTCTTAACAAGACATCCCGTAGTGCTTTTGTGGATGCTGACA	1259
Db	1201	CATTTAAGAAGCTTAGACTCTTCTTAACAAGACATCCCGTAGTGCTTTTGTGGATGCTGACA	1260
Qy	1260	TGTACACGCTCTCTGTGAAGACCTGCGAGCGTAGCTGTTGGTGTCTGCAAGCTTCAAGA	1319
Db	1261	TGTACACGCTCTCTGTGAAGACCTGCGAGCGTAGCTGTTGGTGTCTGCGAGCTTCAAGA	1320
Qy	1320	TAAATGATTTAAGAGCTCTGTGATGTCATACCAATATATATGATCATGACAAGAGAGCCCT	1379
Db	1321	TAAATGATTTAAGAGCTCTGTGATGTCATACCAATATATGATCATGACAAGAGAGCCCT	1380
Qy	1380	TAAAGAGTGAACACAGAGTACTCAGTTGATCTCGAAGACCGGCCCCCAAAAGGCTCTGT	1439
Db	1381	TAAAGAGTGAACACAGAGTACTCAGTTGATCTCGAAGACCGGCCCCCAAAAGGCTCTGT	1440
Qy	1440	ATTCCAGAGCCATGGAATCCATCCAGGAGAGGCTCGACGGGGTGTGATCCATGAGACTG	1499
Db	1441	ATTCCAGAGCCATGGAATCCATCCAGGAGAGGCTCGACGGGGTGTGATCCATGAGACTG	1500
Qy	1500	ATGACCATATGGGTGGCATCCCTGCCCCGGAATATGTAAGGGGAAAAGGCTTCTGCTTATA	1559
Db	1501	ATGACCATATGGGTGGCATCCCTGCCCCGGAATATGTAAGGGGAAAAGGCTTCTGCTTATA	1560
Qy	1560	TTGGATCATATGACATTCCTACAGTCTTACAGTTTGTATAGAAAGTTGAGAGCACTTTGGA	1619
Db	1561	TTGGATCATATGACATTCCTACAGTCTTACAGTTTGTATAGAAAGTTGAGAGCACTTTGGA	1620
Qy	1620	AAGCCCTGGTACATGACCGGAGACACTGTCTCAGTGCACTGCCCAGGCTTCTACGCTGAC	1679
Db	1621	AAGCCCTGGTACATGACCGGAGACACTGTCTCAGTGCACTGCCCAGGCTTCTACGCTGAC	1680
Qy	1680	GGTTCACAGGCTTCAATGTGCAACACAGATTTTAAAGATTTCCCTTGAAGCTTCTCTT	1739
Db	1681	GGTTCACAGGCTTCAATGTGCAACACAGATTTTAAAGATTTCCCTTGAAGCTTCTCTT	1740
Qy	1740	CCAAAAGGTTTCGGTCTGAGCTCATCTTCTCGGCGAGAGGCTCGAGTGGCAACTCT	1799
Db	1741	CCAAAAGGTTTCGGTCTGAGCTCATCTTCTCGGCGAGAGGCTCGAGTGGCAACTCT	1800
Qy	1800	GCATTACTTACCAAGCCATCGGTCTCTGGGGAACACAAAGGCAAACTGACAAACAAAGGAG	1859
Db	1801	GCATTACTTACCAAGCCATCGGTCTCTGGGGAACACAAAGGCAAACTGACAAACAAAGGAG	1860
Qy	1860	AAGTGAAGCCAGGCGCTTCACTTGGTGGTCTCTGATGTTTATCTCAACTCACCCTTTGG	1919
Db	1861	AAGTGAAGCCAGGCGCTTCACTTGGTGGTCTCTGATGTTTATCTCAACTCACCCTTTGG	1920
Qy	1920	AAGAAATCAGTGAAGGGCTCGCCTATTCCTGAACCCAGTTTCTCACCTCAGTGGAGAGA	1979
Db	1921	AAGAAATCAGTGAAGGGCTCGCCTATTCCTGAACCCAGTTTCTCACCTCAGTGGAGAGA	1980
Qy	1980	CTTTGCAAAATGCTAATCAATCAAGTACAACTTGGAAAACCTTGAAGTTGACAGTCAAGT	2039
Db	1981	CTTTGCAAAATGCTAATCAATCAAGTACAACTTGGAAAACCTTGAAGTTGACAGTCAAGT	2040
Qy	2040	TCACCCATTAAAGCGAAAGCTCAGAAAGACTGAAACAAGATTCTGCCATCTCTGTATC	2099
Db	2041	TCACCCATTAAAGCGAAAGCTCAGAAAGACTGAAACAAGATTCTGCCATCTCTGTATC	2100
Qy	2100	CCAAAGTGTACAGCCCTTGTGCCCGAGCAATGTGAATTTTCTTACTGTGTCATCAAAAAA	2159
Db	2101	CCAAAGTGTACAGCCCTTGTGCCCGAGCAATGTGAATTTTCTTACTGTGTCATCAAAAAA	2160
Qy	2160	GGAGTGTATTAAGAATGAGGGGAGCTGCTCCTCAATCTTCTTCTGGAAGAAACCTTCT	2219
Db	2161	GGAGTGTATTAAGAATGAGGGGAGCTGCTCCTCAATCTTCTTCTGGAAGAAACCTTCT	2220
Qy	2220	CTCTCTTCTCTTCTCATGATGGGCTTATGCTCTCAGAGAGTTTGAGAGCCGACGATC	2279

Db 2453 CTTTGCAAAAGCTAAGTACAGTAAACCTTGAAAAAGCTTGAAGTTGCAGAGTCAAGT 2512
 Qy 2040 TCACCCATTAAAGCGAAGGCTCAGAGAGCTGGAACAAGTTTCCCATCTGTGATC 2099
 Db 2513 TCACCCATTAAAGCGAAGGCTCAGAGAGCTGGAACAAGTTTCCCATCTGTGATC 2572
 Qy 2100 CCAAGATGTCAGCCCTTGCCCGAGCAATGTGAATTTTCTCTCATCTGTGATCAAAAA 2159
 Db 2573 CCAAGATGTCAGCCCTTGCCCGAGCAATGTGAATTTTCTCTCATCTGTGATCAAAAA 2632
 Qy 2160 GAGGTGAATGAAGTGAAGGAGCTGCTCCATCTTCTCTCTGAAGAAACCTTCT 2219
 Db 2693 GAGGTGAATGAAGTGAAGGAGCTGCTCCATCTTCTCTCTGAAGAAACCTTCT 2692
 Qy 2220 CTCCTTCTCTCTCATGAATGGGCTTGAAGCTCAGAGAGTTGAGAGCCGAGCATC 2279
 Db 2693 CTCCTTCTCTCTCATGAATGGGCTTGAAGCTCAGAGAGTTGAGAGCCGAGCATC 2752
 Qy 2280 CCGTCACCTCAGAGTGGGAGTGAAGTTTCACTGGCCAAACCTTGGCTCCTCACTA 2339
 Db 2753 CCGTCACCTCAGAGTGGGAGTGAAGTTTCACTGGCCAAACCTTGGCTCCTCACTA 2812
 Qy 2340 TTGAATTTTTCAGACCCCAATCTTCACTGCTGGAATGGGATGCTGAGCTTGAGC 2399
 Db 2813 TTGAATTTTTCAGACCCCAATCTTCACTGCTGGAATGGGATGCTGAGCTTGAGC 2872
 Qy 2400 TTTCTTTTCCCTCTCTTGAATCCGGAATCTTAACTTCTCTCAGAGAGCTGAGC 2459
 Db 2873 TTTCTTTTCCCTCTCTTGAATCCGGAATCTTAACTTCTCTCAGAGAGCTGAGC 2932
 Qy 2460 TGGCAGATTAATCCCTAAGTCTTCTCTCTGAGCTCTGGAAGAAATCTCTGTAAT 2519
 Db 2993 TGGCAGATTAATCCCTAAGTCTTCTCTCTGAGCTCTGGAAGAAATCTCTGTAAT 2992
 Qy 2520 CTCTGTAAGGTTTTTGGGGGATAAGGGGTTTAAACAAGCTCCAGCTTCTCTCTT 2579
 Db 2993 CTCTGTAAGGTTTTTGGGGGATAAGGGGTTTAAACAAGCTCCAGCTTCTCTCTT 3052
 Qy 2580 TTTTCTTGAAGAAAGGAAAAAGCAACAAGCAACAATTTCAAGCATTTTCAGATCG 2639
 Db 3053 TTTTCTTGAAGAAAGGAAAAAGCAACAAGCAACAATTTCAAGCATTTTCAGATCG 3112
 Qy 2640 AACTCCAGAGTGTGACAAAGATGCTTATCTGAGATTCCTCAGAGAGCCATGATG 2699
 Db 3113 AACTCCAGAGTGTGACAAAGATGCTTATCTGAGATTCCTCAGAGAGCCATGATG 3172
 Qy 2700 TTATGAAGAGAGAGTGAATGCTTCTCTGCGAGAGAGCTCTCTTAACTCTCTCTC 2759
 Db 3173 TTATGAAGAGAGAGTGAATGCTTCTCTGCGAGAGAGCTCTCTTAACTCTCTCTC 3232
 Qy 2760 TCTGTGAATTTCTTAAGGCTGAAGAGTAAGAGAGTGGGAGCATGGGATATCTTAT 2819
 Db 3233 TCTGTGAATTTCTTAAGGCTGAAGAGTAAGAGAGTGGGAGCATGGGATATCTTAT 3292
 Qy 2820 CCGCTTTGTTAAAGAGAGGAGCCATGGGCTGGAGATCATAGCCCTTCTAGGAGCA 2879
 Db 3293 CCGCTTTGTTAAAGAGAGGAGCCATGGGCTGGAGATCATAGCCCTTCTAGGAGCA 3352
 Qy 2880 ATCCCTTGAAGGAGGAGGAGTGAATTAATTTTGAATTTGAATTAATTTCTG 2939
 Db 3353 ATCCCTTGAAGGAGGAGGAGTGAATTAATTTTGAATTTGAATTAATTTCTG 3412
 Qy 2940 GTTGTGTTTCTTAATGTAAGACTTACCAATGAAATTTAGATCATCTTCTCAGAGAGAT 2999
 Db 3413 GTTGTGTTTCTTAATGTAAGACTTACCAATGAAATTTAGATCATCTTCTCAGAGAGAT 3472
 Qy 3000 TTTTGTCTCTCTCACTTTTCCAAAGTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGT 3059
 Db 3473 TTTTGTCTCTCTCACTTTTCCAAAGTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGT 3532
 Qy 3060 AGGGGACACTTGT 3119
 Db 3533 AGGGGACACTTGT 3592

Qy 3120 TTAAGCTAATGGGAGAGCAGAGATTTCTGCTTGTGTGAGTCAATGCTGTGCAATATGT 3179
 Db 3593 TTAAGCTAATGGGAGAGCAGAGATTTCTGCTTGTGTGAGTCAATGCTGTGCAATATGT 3652
 Qy 3180 CCTAACCCCTGTCTTATGAGAGGAGTGAATGGGGGCTACATATGCTCTCTCTC 3239
 Db 3653 CCTAACCCCTGTCTTATGAGAGGAGTGAATGGGGGCTACATATGCTCTCTCTC 3712
 Qy 3240 CCGGTCTAAGAGT 3299
 Db 3713 CCGGTCTAAGAGT 3772
 Qy 3300 GGGCTGTGATCTCAGAGATTTGTAATTCCTGTGTATCCCTTCTATCCACCT 3359
 Db 3773 GGGCTGTGATCTCAGAGATTTGTAATTCCTGTGTATCCCTTCTATCCACCT 3832
 Qy 3360 GCGTGAATATGTTAGCCCATACCCCAATACCTGTCTATTTAGACACCCCGCA 3419
 Db 3833 GCGTGAATATGTTAGCCCATACCCCAATACCTGTCTATTTAGACACCCCGCA 3892
 Qy 3420 GTTCTGAGCTGCTGT 3479
 Db 3893 GTTCTGAGCTGCTGT 3952
 Qy 3480 TTTTCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3539
 Db 3953 TTTTCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4012
 Qy 3540 GTTGGGAGTGAAGAGAAATTTGAAGGAGGCTGGCTTGAAGAAAGAAATGGGAG 3599
 Db 4013 GTTGGGAGTGAAGAGAAATTTGAAGGAGGCTGGCTTGAAGAAAGAAATGGGAG 4072
 Qy 3600 CAACATTTTATTAAGTGTACTTATTTGCTCTACTTGTGTATTTGTCAGAAATGGCAAT 3659
 Db 4073 CAACATTTTATTAAGTGTACTTATTTGCTCTACTTGTGTATTTGTCAGAAATGGCAAT 4132
 Qy 3660 ACAATATTAAGTGTATGATGTTTATGATTAATTAATTAATTAATTAATTAATTA 3713
 Db 4133 ACAATATTAAGTGTATGATGTTTATGATTAATTAATTAATTAATTAATTAATTA 4186

RESULT 5
 US-60-324-185-24985
 ; Sequence 24985, Application US/60324185
 ; GENERAL INFORMATION:
 ; APPLICANT: Morris, MacDonald
 ; APPLICANT: Lal, Preeti
 ; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
 ; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
 ; FILE REFERENCE: GX-0019-1 P
 ; CURRENT APPLICATION NUMBER: US/60/324,185
 ; NUMBER OF SEQ ID NOS: 35862
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 24985
 ; LENGTH: 3720
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incycle ID No: 348086.13
 US-60-324-185-24985

Query Match 99.3%; Score 3688; DB 76; Length 3720;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 3711; Conservative 0; Mismatches 0; Indels 3; Gaps 2;

Qy 1 ATTAACAGGCGCTGTGTTAGAGAGCAGAGAGAGGCGCTTGTGCTTGTGAGACTTTTCA 60
 Db 1 ATTAACAGGCGCTGTGTTAGAGAGCAGAGAGAGGCGCTTGTGCTTGTGAGACTTTTCA 60